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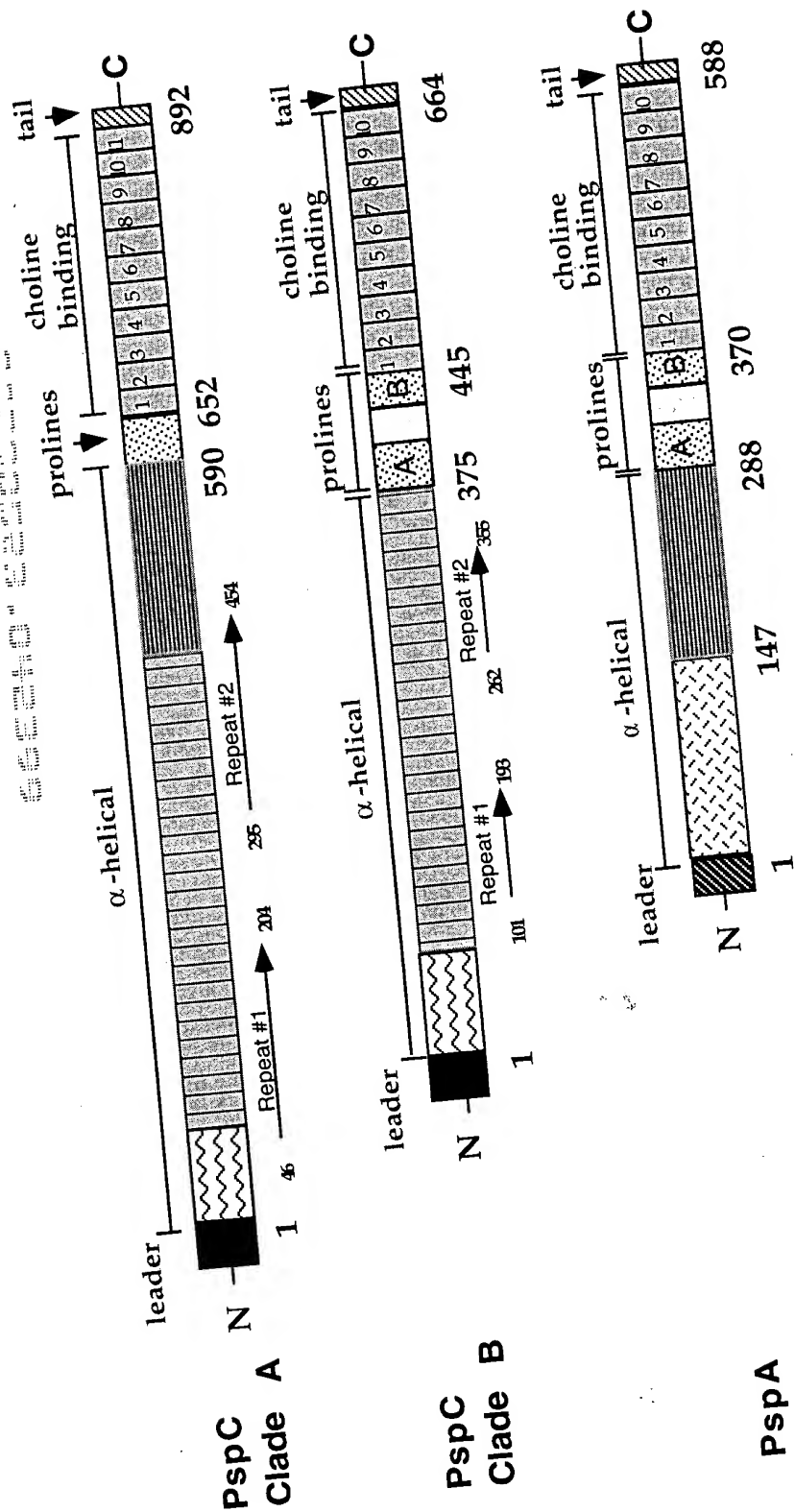
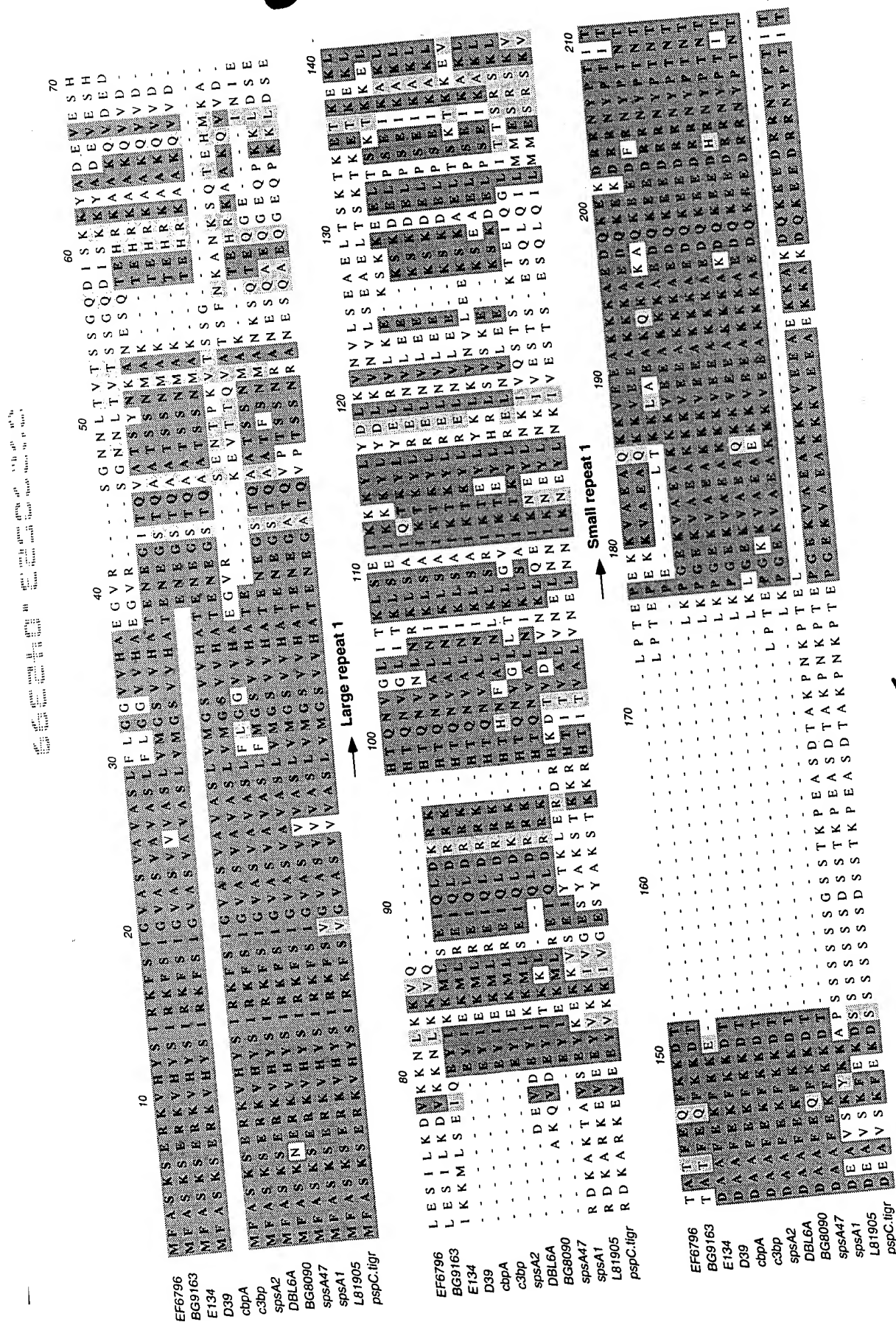
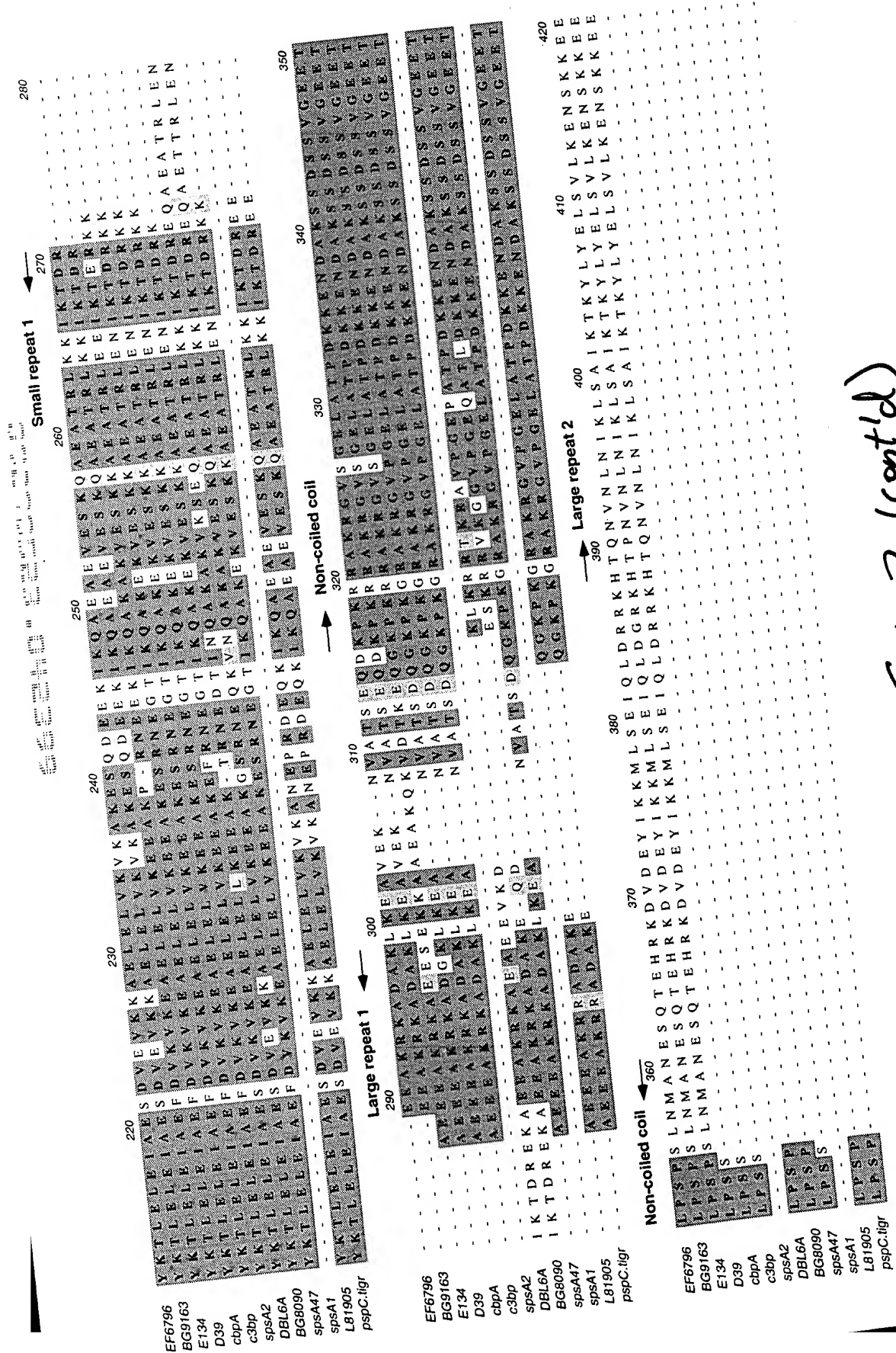


Figure 1: Cartoon of the PspC Clades compared to a representative PspA molecule. Long arrows represent the direct repeats found within PspA molecule. The hypervariable region is indicated by the zig-zag lines. The region of homology found with the alpha helix is indicated by the horizontal lines.

Fig. 1





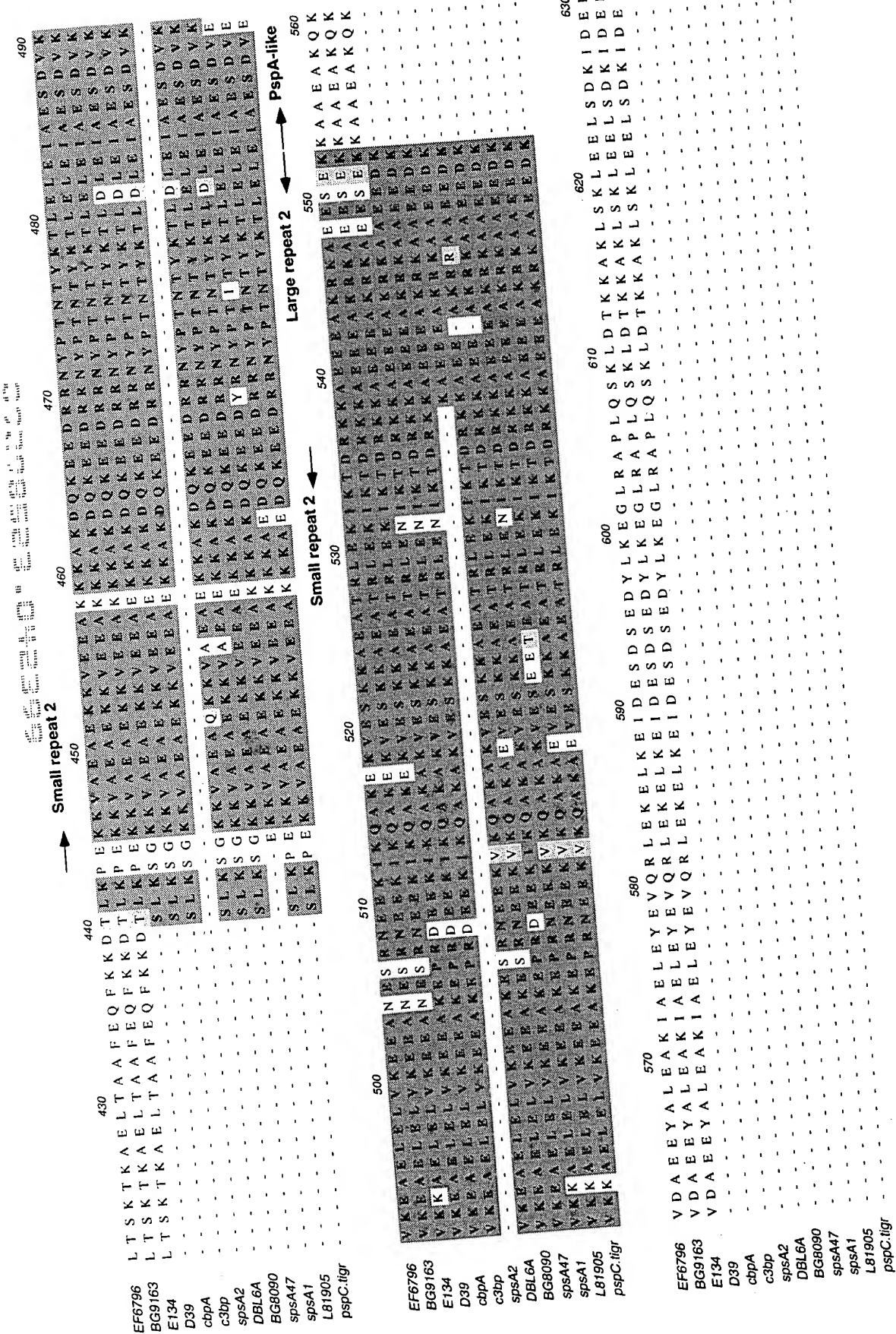


Fig. 2 (cont'd)

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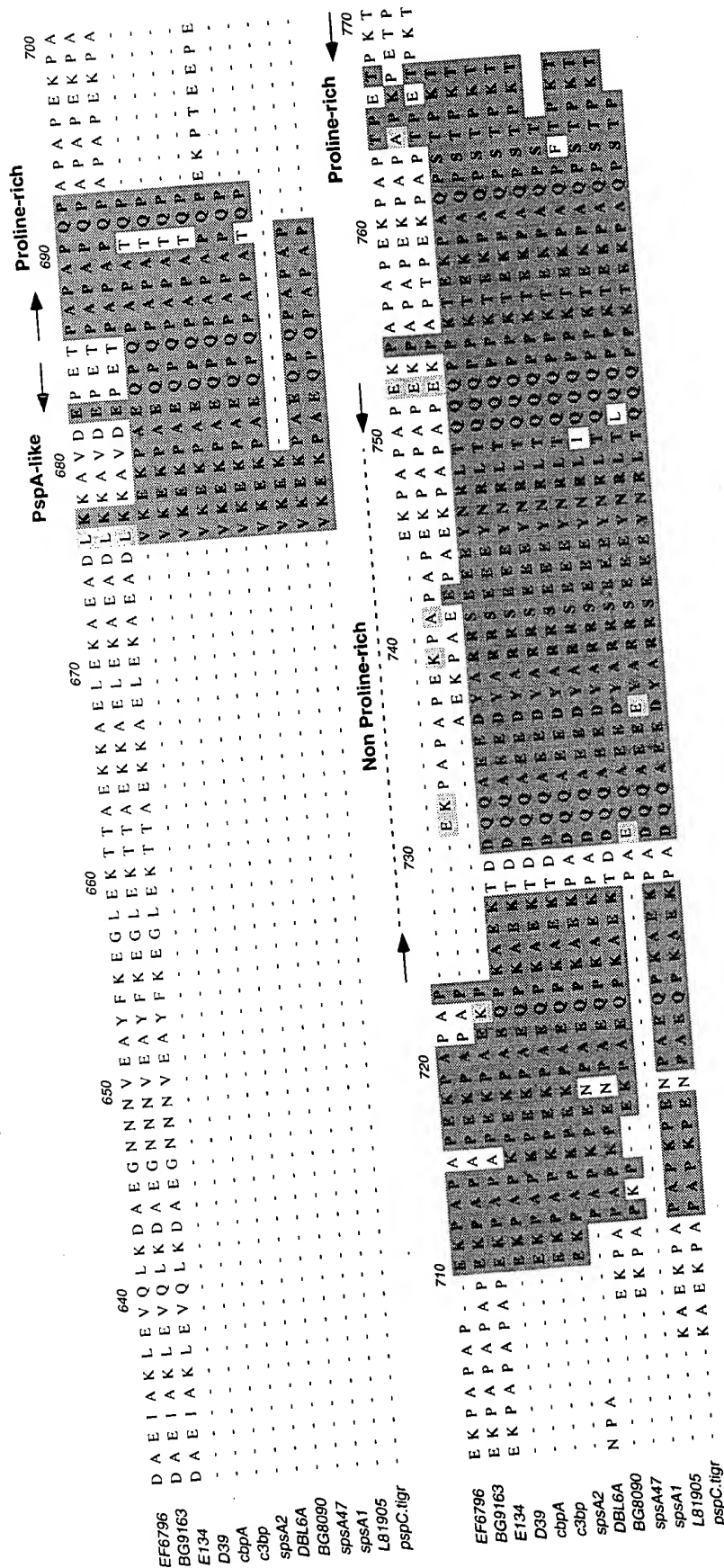


Fig. 2 (cont'd)

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	a	b	c	d	e	f	g	
1								Glu Gly Val Arg Ser Gly Asn Asn Leu Thr
11								Val Thr Ser Ser Gly
16		Gln	Asp	Ile	Ser	Lys	Lys	
22	Tyr	Ala	Asp	Glu	Val	Glu	Ser	
29		His	Leu	Glu	Ser	Ile		
34	Leu	Lys	Asp	Val	Lys	Lys	Asn	
41	Leu	Lys	Lys					
44	Val	Gln	His	Thr	Gln	Asn	Val	
51		Gly	Leu	Ile	Thr	Lys		
56	Leu	Ser	Glu	Ile	Lys	Lys	Lys	
63							Tyr	
64	Leu	Tyr	Asp	Leu	Lys			
69	Val	Asn	Val	Leu	Ser	Glu	Ala	
76		Glu	Leu	Thr	Ser	Lys		
81			Thr	Lys	Glu	Thr		
85	Lys	Glu	Lys	Leu	Thr	Ala	Thr	
92	Phe	Glu	Gln	Phe	Lys	Lys	Asp	
99								Thr Leu Pro Thr Glu Pro
105				Glu	Lys	Lys		
108	Val	Ala	Glu	Ala	Gln	Lys	Lys	
115	Val	Glu	Glu	Ala	Lys	Lys	Lys	
122			Ala	Glu	Asp	Gln		
126	Lys	Glu	Lys	Asp	Arg	Arg	Asn	
133	Tyr	Pro	Thr	Ile	Thr			
138	Tyr	Lys	Thr	Leu	Glu	Leu	Glu	
145	Ile	Ala	Glu	Ser	Asp	Val	Glu	
152	Val	Lys	Lys	Ala	Glu	Leu	Glu	
159	Leu	Val	Lys	Val	Lys	Ala	Lys	
166	Glu	Ser	Gln	Asp	Glu	Glu	Lys	
173	Ile	Lys	Gln	Ala	Glu	Ala	Glu	
180	Val	Glu	Ser	Lys	Gln	Ala	Glu	
187			Ala	Thr	Arg			
190	Leu	Lys	Lys	Ile	Lys	Thr	Asp	
197	Arg	Glu	Glu	Ala	Lys	Arg	Lys	
204		Ala	Asp	Ala	Lys	Leu	Lys	
210		Glu	Ala	Val	Glu	Lys	Asn	
216	Val	Ala	Thr	Ser	Glu	Gln	Asp	
223	Lys							
224								Pro Lys Arg Arg Ala Lys Arg Gly Val Ser
234								Gly Glu Leu Ala Thr Pro Asp Lys Lys Glu
244								Asn Asp Ala Lys Ser Ser Asp Ser Ser Val
254								Gly Glu Glu Thr Leu Pro Ser Pro Ser Leu
264								Asn Met Ala Asn
268				Glu	Ser	Gln		
271		Thr	Glu	His	Arg	Lys	Asp	
277	Val	Asp	Glu	Tyr				
281	Ile	Lys	Lys	Met	Leu	Ser	Glu	
288	Ile	Gln	Leu	Asp	Arg	Arg	Lys	
295		His	Thr	Gln	Asn	Val		
300		Asn	Leu	Asn	Ile	Lys		
305	Leu	Ser	Ala	Ile	Lys	Thr	Lys	
312			Tyr	Leu	Tyr	Glu		
316	Leu	Ser	Val	Leu	Lys	Glu	Asn	
323				Ser	Lys			
325	Lys	Glu	Glu	Leu	Thr	Ser	Lys	
332			Thr	Lys	Ala	Glu		
336	Leu	Thr	Ala	Ala	Phe	Glu	Gln	

FIG. 3

page 1



343	Phe Lys Lys	
346		Asp Thr Leu Lys Pro
351		Glu Lys Lys
354	Val Ala Glu Ala Glu Lys Lys	
361	Val Glu Glu Ala Lys Lys Lys	
368		Ala Lys Asp Gln
372	Lys Glu Glu Asp Arg Arg Asn	
379		Tyr
380		Pro Thr Asn Thr
384	Tyr Lys Thr Leu Glu Leu Glu	
391	Ile Ala Glu Ser Asp Val Lys	
398	Val Lys Glu Ala Glu	
403	Leu Glu Leu Val Lys Glu Glu	
410	Ala Asn Glu Ser Arg Asn Glu	
417		Glu Lys Ile Lys Gln Ala
423	Lys Glu Lys Val Glu Ser Lys	
430	Lys Ala Glu Ala Thr Arg	
436	Leu Glu Lys Ile Lys Thr Asp	
443	Arg Lys Lys Ala Glu Glu Glu	
450		Ala Lys Arg Lys
454	Ala Glu Glu Ser Glu Lys Lys	
461	Ala Ala Glu Ala Lys Gln Lys	
468	Val Asp Ala Glu Glu Tyr Ala	
475		Leu Glu Ala Lys
479	Ile Ala Glu Leu Glu Tyr Glu	
486	Val Gln Arg Leu Glu Lys Glu	
493	Leu Lys Glu	
496	Ile Asp Glu Ser Asp Ser Glu	
503		Asp Tyr Leu Lys Glu Gly
509	Leu Arg Ala	
512		Pro Leu Gln Ser Lys
517	Leu Asp Thr Lys Lys Ala Lys	
524	Leu Ser Lys	
527	Leu Glu Glu Leu Ser Asp Lys	
534	Ile Asp Glu Leu Asp Ala Glu	
541	Ile Ala Lys Leu Glu Val Gln	
548	Leu Lys Asp Ala Glu Gly Asn	
555		Asn Asn
557	Val Glu Ala Tyr Phe Lys Glu	
564		Gly Leu Glu Lys Thr
569		Thr Ala Glu Lys Lys
574	Ala Glu Leu Glu Lys Ala	
580	Glu Ala Asp Leu Lys Lys Ala	
587	Val Asp Glu	

**Figure 3.** The coiled-coil motif of the  $\alpha$ -helix of PspC. Amino acids that are not in the coiled-coil motif are in the right column. This is the output from the Matcher program accessed through the Internet (<http://catt.poly.edu/~jps/>).

Fig. 3 (cont'd)

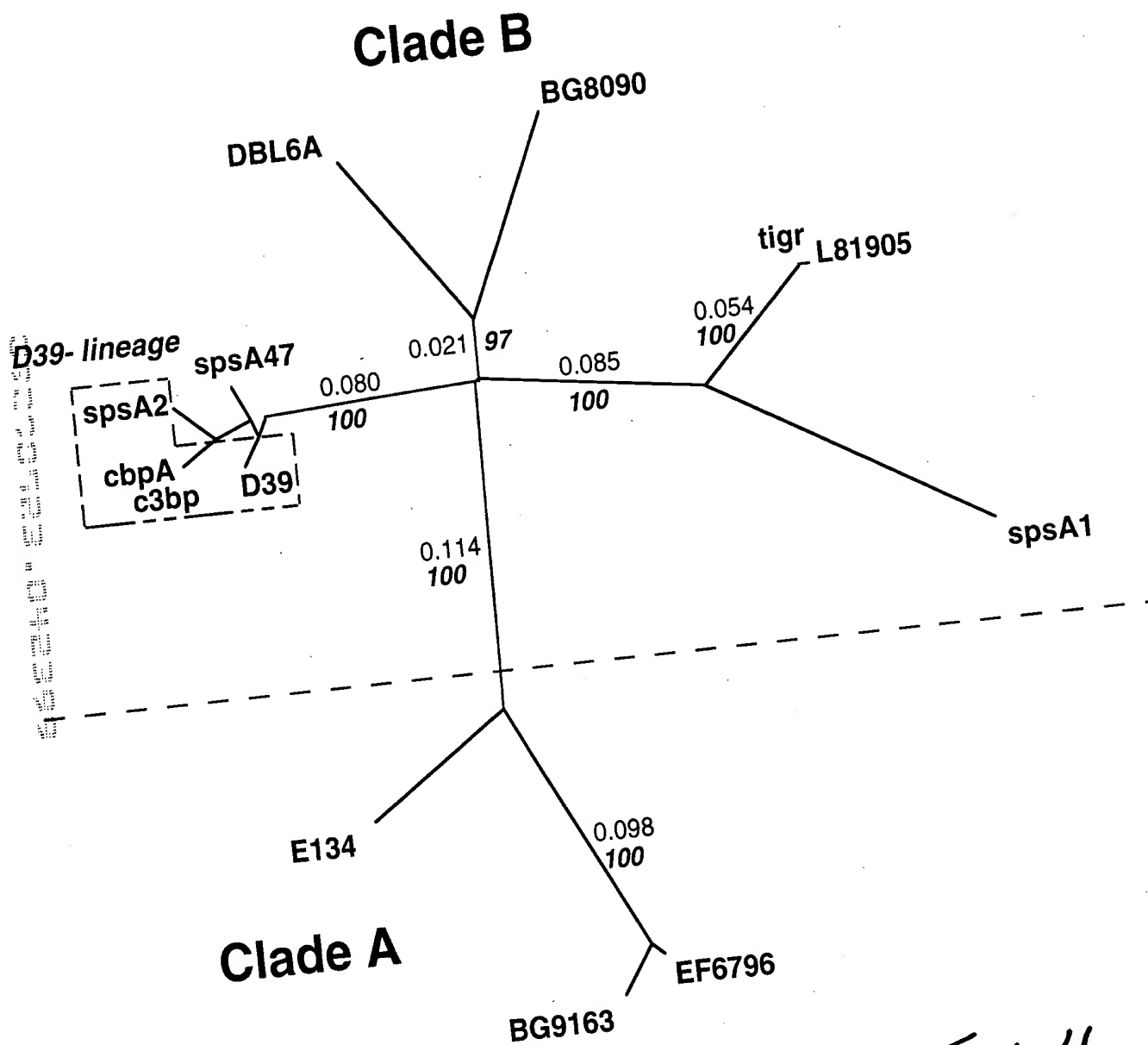


Fig. 4



FIGURE 5. Choline-binding Domain

PspC consensus

11111111112  
12345678901234567890  
1 KTGWKQENGWYFYNTDGSMA  
2 TGLQNNNGSWYYLNAMGAMA  
3 TGLQNNNGSWYYLNANGSMA  
4 TGLQNNNGSWYYLNANGAMA  
5 TGLQYNGSWYYLNANGDMA  
6 TGLQYNGSWYYLNSNGAMA  
7 TGLQYNGSWYYLNANGDMA  
8 TGLQNNNGSWYYLNANGDMA  
9 TGLQYN SWYYLNANGDMA  
10 TGWVKDGDWYYLEASGAMKA  
11 SQWFKVSDKWYYVNGSGALA

VNTTVDGYGVNANGWVN 18 amino acid tail PspC  
28% identical to consensus

TGLQNNNGSWYYLNANGAMA PspC consensus repeat  
Y

For PspA/R36A alignment see Yother and Briles 1992.

TGLQXNGSWYYLNANGAMA PspA/Rx1 consensus  
Y 95% identical to PspC consensus

VNTTVDGYKVNANGWV\_ PspA/Rx1 17 amino acid tail.  
One AA different from PspC,  
And one AA shorter.

Fig. 5

PspA/EF5668

11111111112

12345678901234567890

1 IGWKQENGMWYFYNTDGSM A  
2 TGWLQNNGSWYYLNSNGAM A  
3 TGWLQYNGSWYYLNANGAM A  
4 TGWLQYNGSWYYLNANGAM A  
5 TGWLQYNGSWYYLNANGDM A  
6 TGWLQYNGSWYYLNANGDM A  
7 TGWAKVHGSWYYLNANGSM A  
8 TGWVKDGETWYYLEASGSMKA  
9 NQWFQVSDKWYYVNGLGSL S  
10 VNTTVDGYKVNANGEWV

17 amino acid tail EF5668 PspA

TGWLQYNGSWYYLNANGSM A

PspA/EF5668 consensus

90% identical to PspC consensus

#### Repeat #1

PspC consensus

KTGWKQENGNWYFYNTDGSM A

PspA/Rx1

TGWKQENGMWYFYNTDGSM A

PspA/EF5668

IGWKQENGMWYFYNTDGSM A

#### Repeat #N-1

PspC consensus

TGWVKDGDWYYLEASGAMKA

PspA/Rx1

TGWVKDGDWYYLEASGAMKA

PspA/EF5668

TGWVKDGETWYYLEASGSMKA

#### Repeat #N

PspC consensus

SQWFKVSDKWYYVNGSGALA

PspA/Rx1

SQWFKVSDKWYYVNGLGALA

PspA/EF5668

NQWFQVSDKWYYVNGLGSL S

#### 17-18 AA tail

PspC consensus

VNTTVDGYGVNANGEWVN

PspA/Rx1

VNTTVDGYKVNANGEWV

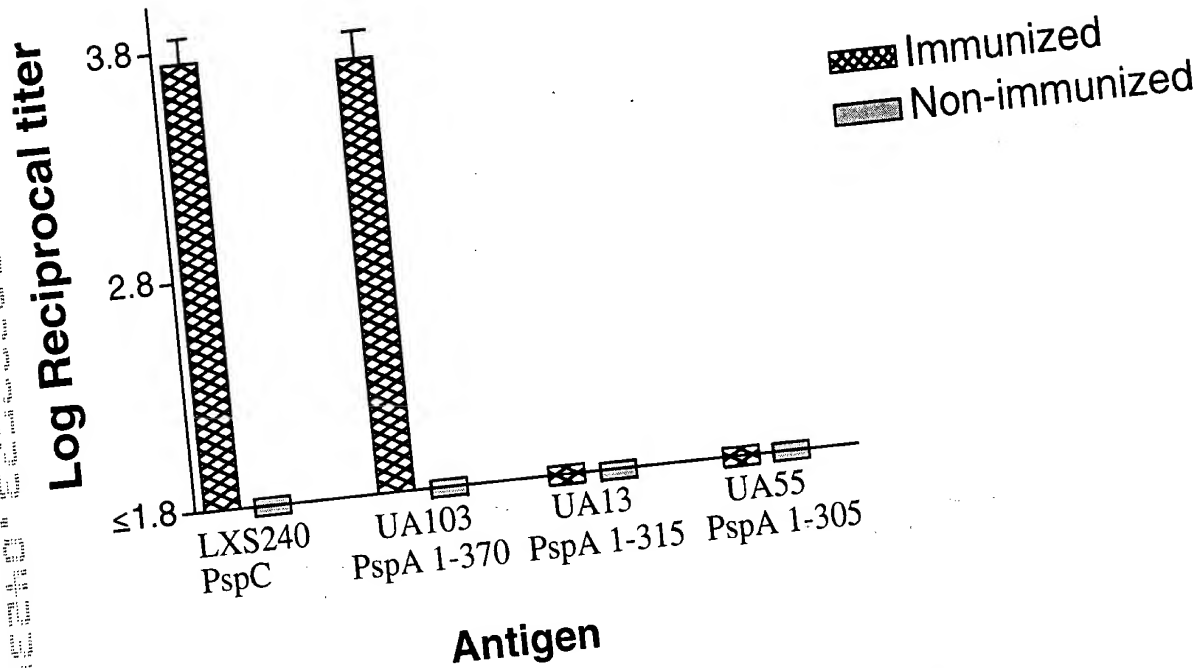
PspA/EF5668

VNTTVDGYKVNANGEWV

Fig. 5 (cont'd)

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# Log Reciprocal titer of serum from PspC-immunized mice



**Figure 7.** Level of antibody reactive to PspC and PspA fragments present in the sera of mice immunized with PspC. Each bar represents the mean of the log reciprocal titer and upperbound of standard error of sera from five mice. The limit of detection of the log reciprocal antibody titer is 1.8.

FIG. 7

Fig. 8

Other Formats:

Links:

LOCUS CAA05158 539 aa BCT 14-OCT-1997  
 DEFINITION SpsA protein.  
 ACCESSION CAA05158  
 PID g2576331  
 VERSION CAA05158.1 GI:2576331  
 DBSOURCE embl locus SPSPSA2, accession AJ002054.1  
 KEYWORDS  
 SOURCE Streptococcus pneumoniae.  
 ORGANISM Streptococcus pneumoniae  
 Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
 Streptococcus.  
 REFERENCE 1 (residues 1 to 539)  
 AUTHORS Hammerschmidt,S.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-OCT-1997) Hammerschmidt S., Microbiology, Division  
 Microbial Pathogenesis, National Research Centre for Biotechnology,  
 Spielmannstrasse 7, 38106 Braunschweig, GERMANY  
 REFERENCE 2 (residues 1 to 539)  
 AUTHORS Hammerschmidt,S., Talay,S.R., Brandtzaeg,P. and Chhatwal,G.S.  
 TITLE SpsA, a novel pneumococcal surface protein with specific binding to  
 secretory immunoglobulin A and secretory component  
 JOURNAL Mol. Microbiol. 25 (6), 1113-1124 (1997)  
 MEDLINE 98010350  
 FEATURES Location/Qualifiers  
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 121 akldaafekf kkdtklpgke vaeakkkvee akkkaedqke edrnpytnt yktleleiae  
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the above report in format

Other Formats:

Links:

LOCUS SPSPSA2 1620 bp DNA BCT 14-OCT-1997

DEFINITION Streptococcus pneumoniae SIgA binding.

ACCESSION AJ002054

NID g2576330

VERSION AJ002054.1 GI:2576330

KEYWORDS SpsA protein.

SOURCE Streptococcus pneumoniae.

ORGANISM Streptococcus pneumoniae

Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
Streptococcus.

REFERENCE 1 (bases 1 to 1620)

AUTHORS Hammerschmidt,S.

TITLE Direct Submission

JOURNAL Submitted (13-OCT-1997) Hammerschmidt S., Microbiology, Devison  
Microbial Pathogenesis, National Research Centre for Biotechnology,  
Spielmannstrasse 7, 38106 Braunschweig, GERMANY

REFERENCE 2 (bases 1 to 1620)

AUTHORS Hammerschmidt,S., Talay,S.R., Brandtzaeg,P. and Chhatwal,G.S.

TITLE SpsA, a novel pneumococcal surface protein with specific binding to  
secretory immunoglobulin A and secretory component

JOURNAL Mol. Microbiol. 25 (6), 1113-1124 (1997)

MEDLINE 98010350

FEATURES Location/Qualifiers

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KKA

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PAEQ

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repeat\_region 961..1564

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661 acaaggttag aaaacatcaa gacagatcgt aaaaaagcag aagaagaagc taaacgaaaa  
721 gcagcagaag aagataaagt taaagaaaaa ccagctgaac aaccacaacc agcgccggct  
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Fig. 9

Other Formats:

Links:

LOCUS CAA05159 581 aa BCT 14-OCT-1997

DEFINITION SpsA protein.

ACCESSION CAA05159

PID g2576333

VERSION CAA05159.1 GI:2576333

DBSOURCE embl locus SPSPSA47, accession AJ002055.1

KEYWORDS

SOURCE Streptococcus pneumoniae.

ORGANISM Streptococcus pneumoniae

Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
Streptococcus.

REFERENCE 1 (residues 1 to 581)

AUTHORS Hammerschmidt,S.

TITLE Direct Submission

JOURNAL Submitted (13-OCT-1997) Hammerschmidt S., Microbiology, Division  
Microbial Pathogenesis, National Research Centre for Biotechnology,  
Spielmannstrasse 7, 38106 Braunschweig, GERMANY

REFERENCE 2 (residues 1 to 581)

AUTHORS Hammerschmidt,S., Talay,S.R., Brandtzaeg,P. and Chhatwal,G.S.

TITLE SpsA, a novel pneumococcal surface protein with specific binding to  
secretory immunoglobulin A and secretory component

JOURNAL Mol. Microbiol. 25 (6), 1113-1124 (1997)

MEDLINE 98010350

FEATURES Location/Qualifiers

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Protein 1..581  
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/product="SpsA protein"  
CDS 1..581  
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/coded\_by="AJ002055.1:1..1746"  
/transl\_table=11

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Fig. 9 (cont'd)

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Fig. 9 (cont'd)

page 3

Other Formats:

Links:

LOCUS SPSPSA47 1746 bp DNA BCT 14-OCT-1997

DEFINITION Streptococcus pneumoniae SIgA binding.

ACCESSION AJ002055

NID g2576332

VERSION AJ002055.1 GI:2576332

KEYWORDS SpsA protein.

SOURCE Streptococcus pneumoniae.

ORGANISM Streptococcus pneumoniae

Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;  
Streptococcus.

REFERENCE 1 (bases 1 to 1746)

AUTHORS Hammerschmidt,S.

TITLE Direct Submission

JOURNAL Submitted (13-OCT-1997) Hammerschmidt S., Microbiology, Division  
Microbial Pathogenesis, National Research Centre for Biotechnology,  
Spielmannstrasse 7, 38106 Braunschweig, GERMANY

REFERENCE 2 (bases 1 to 1746)

AUTHORS Hammerschmidt,S., Talay,S.R., Brandtzaeg,P. and Chhatwal,G.S.

TITLE SpsA, a novel pneumococcal surface protein with specific binding to  
secretory immunoglobulin A and secretory component

JOURNAL Mol. Microbiol. 25 (6), 1113-1124 (1997)

MEDLINE 98010350

FEATURES Location/Qualifiers

source 1..1746

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/strain="type 47"

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CDS 1..1746

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Fig. 9 (cont'd)

page 4

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/rpt\_type=DIRECT

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1741 aactaa

Fig. 9 (cont'd)

the above report in format

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Fig. 90

ther Formats:

Links:

LOCUS AAB70838 663 aa BCT 16-SEP-1997

DEFINITION choline binding protein A.

ACCESSION AAB70838

PID g2425109

VERSION AAB70838.1 GI:2425109

DBSOURCE locus AF019904 accession AF019904.1

KEYWORDS

SOURCE Streptococcus pneumoniae.

ORGANISM Streptococcus pneumoniae

Eubacteria; Firmicutes; Low G+C gram-positive bacteria;

Streptococcaceae; Streptococcus.

REFERENCE 1 (residues 1 to 663)

AUTHORS Rosenow,C., Ryan,P., Weiser,J.N., Johnson,S., Fontan,P.,  
Ortqvist,A. and Masure,H.R.TITLE Contribution of novel choline-binding proteins to adherence,  
colonization and immunogenicity of Streptococcus pneumoniae

JOURNAL Mol. Microbiol. (1997) In press

REFERENCE 2 (residues 1 to 663)

AUTHORS Rosenow,C., Ryan,P., Weiser,J.N., Johnson,S., Fontan,P.,  
Ortqvist,A. and Masure,H.R.

TITLE Direct Submission

JOURNAL Submitted (18-AUG-1997) Infectious Diseases, St. Jude Children's  
Research Hospital, 322 North Lauderdale, Memphis, TN 38105, USA

COMMENT Method: conceptual translation supplied by author.

FEATURES Location/Qualifiers

source 1..663

/organism="Streptococcus pneumoniae"

/strain="R6x"

/db\_xref="taxon:1313"

Protein &lt;1..663

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CDS 1..663

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301 eiaesdvkvk eaelelvkee akeprdeeki kqakakvesk kaeatrleni ktdrkkaeee

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## Other Formats:

## Links:

LOCUS AF019904 2480 bp DNA BCT 22-SEP-1997

DEFINITION Streptococcus pneumoniae choline binding protein A (cbpA) gene,  
partial cds.

ACCESSION AF019904

NID g2425108

VERSION AF019904.1 GI:2425108

## KEYWORDS

SOURCE Streptococcus pneumoniae.

ORGANISM Streptococcus pneumoniae

Eubacteria; Firmicutes; Low G+C gram-positive bacteria;

Streptococcaceae; Streptococcus.

REFERENCE 1 (bases 1 to 2480)

AUTHORS Rosenow,C., Ryan,P., Weiser,J.N., Johnson,S., Fontan,P.,  
Ortvist,A. and Masure,H.R.TITLE Contribution of novel choline-binding proteins to adherence,  
colonization and immunogenicity of Streptococcus pneumoniae

JOURNAL Mol. Microbiol. (1997) In press

REFERENCE 2 (bases 1 to 2480)

AUTHORS Rosenow,C., Ryan,P., Weiser,J.N., Johnson,S., Fontan,P.,  
Ortvist,A. and Masure,H.R.

TITLE Direct Submission

JOURNAL Submitted (18-AUG-1997) Infectious Diseases, St. Jude Children's  
Research Hospital, 322 North Lauderdale, Memphis, TN 38105, USA

## FEATURES Location/Qualifiers

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/organism="Streptococcus pneumoniae"

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Fig 10 (c) (l)

page 4

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NANGDMATG

WLQNNGSWYYLNANGDMATGWLQYNGSWYYLNANGDMATGWVKDGDWY  
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BASE COUNT 933 a 452 c 575 g 520 t

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121 gatagaagaa aacataccca aaatgtcgcc ttaacataa agttgagcgc aattaaaacg  
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661 aaggggcggg caaaacgagg agttcttga gagctagcaa cacctgataa aaaagaaaat  
721 gatcggaagt ctcagattc tagcgtaggt gaagaaactc ttcaaagtc atccctgaaa

Fig 10 (cont'd)

Page 5

781 tcaggaaaa aggtagcaga agctgagaag aaggttgaag aagctgagaa aaaagccaag  
841 gatcaaaaa aagaagatcg ccgtaactac ccaaccaata cttacaaac gcttgacct  
901 gaaattgctg agtccgatgt gaaagttaa gaagcggagc ttgaactagt aaaagaggaa  
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Fig. 11

Other Formats:

Links:

LOCUS AAD00184 929 aa BCT 07-OCT-1996

DEFINITION surface protein C.

ACCESSION AAD00184

PID g4097980

VERSION AAD00184.1 GI:4097980

DBSOURCE locus SPU72655 accession U72655.1

KEYWORDS

SOURCE Streptococcus pneumoniae.

ORGANISM Streptococcus pneumoniae

Eubacteria; Firmicutes; Low G+C gram-positive bacteria;

Streptococcaceae; Streptococcus.

REFERENCE 1 (residues 1 to 929)

AUTHORS Brooks-Walter,A., Tart,R.C., Briles,D.E. and Hollingshead,S.K.

TITLE The pspC gene encodes a second pneumococcal surface protein  
homologous to the protection-eliciting PspA protein of  
Streptococcus pneumoniae

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 929)

AUTHORS Brooks-Walter,A., Tart,R.C., Briles,D.E. and Hollingshead,S.K.

TITLE Direct Submission

JOURNAL Submitted (26-SEP-1996) Microbiology, University of Alabama at  
Birmingham, 19th Street South, Box 10, Birmingham, AL 35294-2170,  
USA

FEATURES Location/Qualifiers

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/db\_xref="taxon:1313"

Protein 1..929

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CDS 1..929

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 181 eiaesdvevk kaelelvkvk akesqdeeki kqaeaevesk qaeatrlkki ktdreeakrk  
 241 adakilkeave knvatseqdk pkrakrgvs gelatpdkke ndakssdsv geetlpspsl  
 301 nmanesqteh rkdvdeyikk mlseiqlrr khtqvnlni klsaiktkyl yelsvlkens  
 361 kkeelstktk aeltaafeqf kkdtlkpekk vaeaeckvee akkkakdqke edrmnyptnt  
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1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

Fig. 15 (cont'd)



Links:

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YLY

Fig. 1 (cont'd)

Page 4

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EVE

SKQAEATRLKKIKTDREEAKRKADAKLKEAVEKNVATSEQDKPKRRAKRGVSG  
ELATP

DKKENDAKSSDSSVGEETLPSPSLNMANESQTEHRKDVDEYIKKMLSEIQLDRR  
KHTQ

NVNLNIKLSAIKTKYLYELSVLKENSKEELTSKTKAELTAAFEQFKKDTLKPEK  
KVA

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ANES

RNEEKIKQAKEKVESKKAETRLEKIKTDRKKAEEEEAKRKAEESEKKAEEAKQK  
VDAE

EYALEAKIAELEYEVQRLEKELKEIDESDSELYLKEGLRAPLQSKLDTKKAKLSK  
LEE

LSDKIDELDAEIAKLEVQLKDAEGNNNVEAYFKEGLEKTTAEKKAELEKAEADL  
KKAV

DEPETPAPAPQPAPAPEKPAEKPAPEKPAPEKPAPEKPAPEKPAPEKPAPE  
KP

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WLQNNGSW

YYLNSNGAMATGWLQYNGSWYYLNANGDMATGWLQYNGSWYYLNANGDM  
ATGWFQYNG

SWYYLNANGDMATGWFQYNGSWYYLNANGDMATGWLQYNGSWYYLNSNG  
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NGSWYYLNANGSMATDWVKDGDWYYLEASGAMKASQWFKVSDKWYYVNG  
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TVDSYRVNANGWVN"

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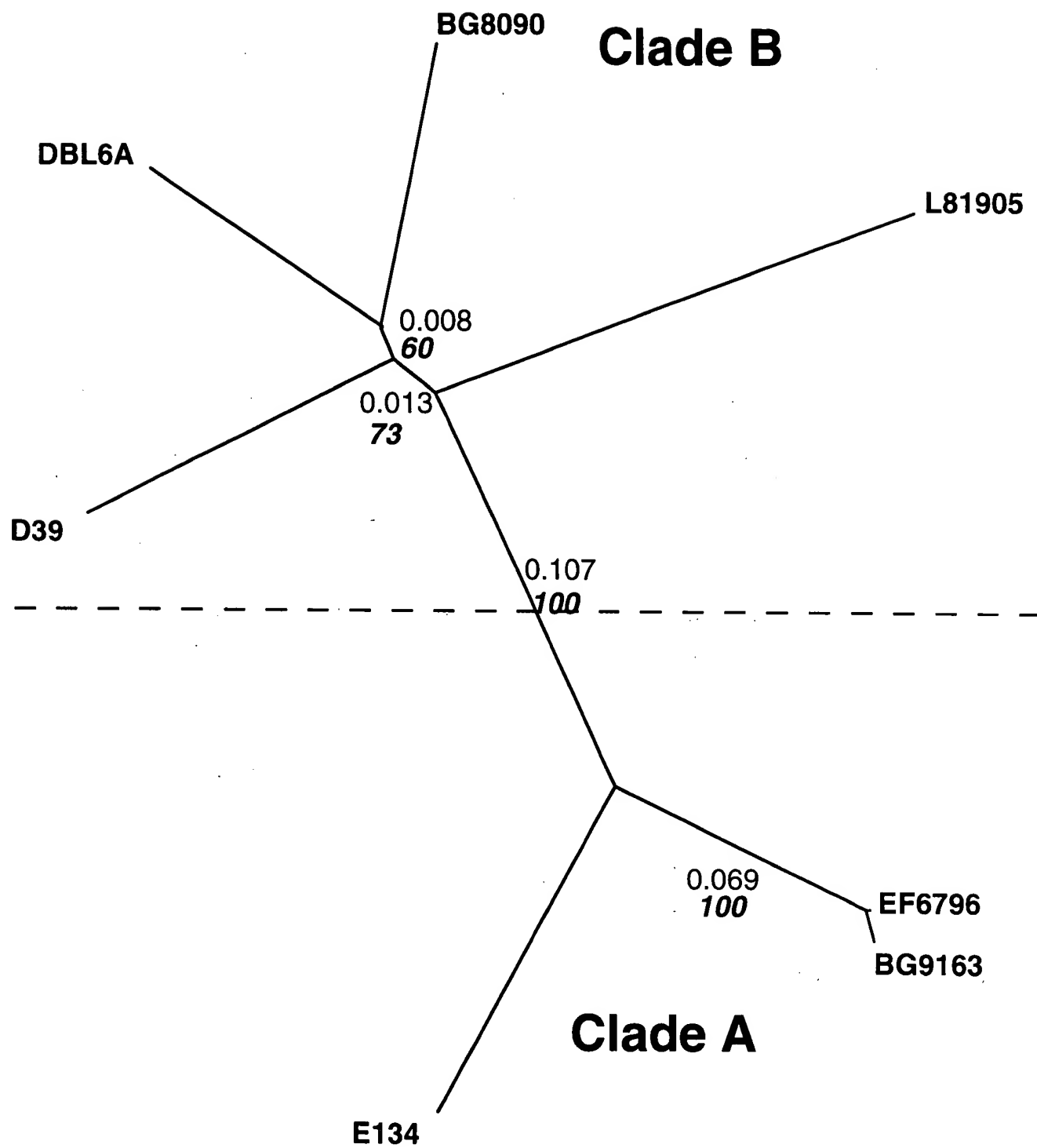
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901 gaactagtaa aagtgaagc taaggaatct caagacgagg aaaaaattaa gcaagcagaa  
961 gcggaagttg agagtaaaaca agctgaggtt acaaggttaa aaaaaatcaa gacagatcgt  
1021 gaagaagcta aacgaaaagc agatgctaag ttgaaggaag ctgttgaaaa gaatgtagcg  
1081 acttcagagc aagataaacc aaagaggcgg gcaaaacgag gagtttctgg agagctagca  
1141 acacctgata aaaaagaaaa tgatgcgaag tcttcagatt ctagcgtagg tgaagaaact  
1201 ctccaagcc catcccttaa tatggcaaat gaaagtcaga cagaacatag gaaagatgtc  
1261 gatgaatata taaaaaaaat gttgagttag atccaattag atagaagaaa acatacccaa  
1321 aatgtcaact taaacataaa gttgagcgca attaaaacga agtatttga tgaattaagt  
1381 gttttaaag agaactcgaa aaaagaagag ttgacgtcaa aaaccaaagc agagttaacc  
1441 gcagcttttg agcagtttaa aaaagataca ttgaaaccag aaaaaaaggt agcagaagct  
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1561 aactaccaa ccaatactta caaaacgctt gaacttgaag ttgctgagtc cgatgtgaag  
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2101 gaagcctact taaagaagg tttagagaaa actactgctg agaaaaaagc tgaattagaa  
2161 aaagctgaag ctgaccttaa gaaagcagtt gatgagccag aaactccagc tccggctcct  
2221 caaccagtc cagctccaga aaaaccagct gaaaaaccag ctccagctcc agaaaaacca  
2281 gctccagtc cagaaaaacc agctccagct ccagaaaaac cagctccagc tccagaaaaa  
2341 ccagctccag ctccagaaaa accagctcca actccagaaa ctccaaaaac aggcttgaaa  
2401 caagaaaacg gtatgtggtg ctctacaat actgatggtt caatggcaac aggctggctc  
2461 caaaacaatg gtcattggtg ctacctcaac agcaatggcg ctatggcgac aggatggctc  
2521 caaaacaatg gtcattggtg ctacctcaac agcaatggcg ctatggcgac aggatggctc  
2581 caatacaatg gttcatggtg ctacctcaac gctaattggtg atatggcgac aggatggctc  
2641 caatacaatg gttcatggtg ctacctcaac gctaattggtg atatggcgac aggatggctc  
2701 caatacaatg gttcatggtg ctacctcaac gctaattggtg atatggcgac aggatggctc  
2761 caatacaatg gttcatggtg ctacctcaac gctaattggtg atatggcgac aggatggctc

2821 caatacaatg gttcatggta ctacctaaac agcaatggg ctatggtaac aggatggctc  
2881 caaaacaatg gctcatggta ctacctaaac gctaacgggt caatggcaac agattgggtg  
2941 aaagatggag atacctggta ctatctgaa gcatcaggtg ctatgaaagc aagccaatgg  
3001 ttcaaagtat cagataaatg gtactatgtc aatggctcag gtgcccttgc agtcaacaca  
3061 actgtagata gctatagagt caatgccaat ggtgaatggg taaactaaac ttaatataac  
3121 tagttaatac tgacttctg taagaactct ttaaagtatt ccctacaaat accatattct  
3181 ttcagtagat aatataacct ttaggaagt ttagattaaa aaataactct gtaattctta  
3241 gccggattta tagcgctaga gactacggag ttttttgat gaggaaagaa tggcggcatt  
3301 caagagactc ttaagagag ttacgggtt taaactatta agctttctcc aattgcaaga  
3361 gggttcaat ctctgctagg tgctagctg cgaaatggct cccacggagt ttggcgcgc  
3421 cagatgttcc acggaggtag tgaggagcga ggccgcggaa ttc

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the above report in format

FIG. 12



— 0.05 changes

UAB pspc align.fasta Formatted Alignments

Fig. 13

# UAB PspC Sequences

EF6796	10	20	30	40	50	60	70
BG9163	11	21	31	41	51	61	71
E134	12	22	32	42	52	62	72
D39	13	23	33	43	53	63	73
DBL6A	14	24	34	44	54	64	74
BG8090	15	25	35	45	55	65	75
L81905	16	26	36	46	56	66	76
EF6796	80	90	100	110	120	130	140
BG9163	81	91	101	111	121	131	141
E134	82	92	102	112	122	132	142
D39	83	93	103	113	123	133	143
DBL6A	84	94	104	114	124	134	144
BG8090	85	95	105	115	125	135	145
L81905	86	96	106	116	126	136	146
EF6796	150	160	170	180	190	200	210
BG9163	151	161	171	181	191	201	211
E134	152	162	172	182	192	202	212
D39	153	163	173	183	193	203	213
DBL6A	154	164	174	184	194	204	214
BG8090	155	165	175	185	195	205	215
L81905	156	166	176	186	196	206	216
EF6796	220	230	240	250	260	270	280
BG9163	221	231	241	251	261	271	281
E134	222	232	242	252	262	272	282
D39	223	233	243	253	263	273	283
DBL6A	224	234	244	254	264	274	284
BG8090	225	235	245	255	265	275	285
L81905	226	236	246	256	266	276	286
EF6796	290	300	310	320	330	340	350
BG9163	291	301	311	321	331	341	351
E134	292	302	312	322	332	342	352
D39	293	303	313	323	333	343	353
DBL6A	294	304	314	324	334	344	354
BG8090	295	305	315	325	335	345	355
L81905	296	306	316	326	336	346	356

UAB pspC align.fasta Formatted Alignments

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360
EF6796 SVGEETLPPSP 360
BG9163 SVGEETLPPSP 360
E134 SVGEETLPPSP 360
D39 SVGEETLPPSP 360
DBL6A SVGEETLPPSP 360
BG8090 SVGEETLPPSP 360
L81905 SVGEETLPPSP 360

370
EF6796 NSKKEELTSKTKAEELTAAFEQFKKDDT 370
BG9163 NSKKEELTSKTKAEELTAAFEQFKKDDT 370
E134 NSKKEELTSKTKAEELTAAFEQFKKDDT 370
D39 NSKKEELTSKTKAEELTAAFEQFKKDDT 370
DBL6A NSKKEELTSKTKAEELTAAFEQFKKDDT 370
BG8090 NSKKEELTSKTKAEELTAAFEQFKKDDT 370
L81905 NSKKEELTSKTKAEELTAAFEQFKKDDT 370

380
EF6796 SVGEETLPPSP 380
BG9163 SVGEETLPPSP 380
E134 SVGEETLPPSP 380
D39 SVGEETLPPSP 380
DBL6A SVGEETLPPSP 380
BG8090 SVGEETLPPSP 380
L81905 SVGEETLPPSP 380

390
EF6796 SVGEETLPPSP 390
BG9163 SVGEETLPPSP 390
E134 SVGEETLPPSP 390
D39 SVGEETLPPSP 390
DBL6A SVGEETLPPSP 390
BG8090 SVGEETLPPSP 390
L81905 SVGEETLPPSP 390

400
EF6796 SVGEETLPPSP 400
BG9163 SVGEETLPPSP 400
E134 SVGEETLPPSP 400
D39 SVGEETLPPSP 400
DBL6A SVGEETLPPSP 400
BG8090 SVGEETLPPSP 400
L81905 SVGEETLPPSP 400

410
EF6796 SVGEETLPPSP 410
BG9163 SVGEETLPPSP 410
E134 SVGEETLPPSP 410
D39 SVGEETLPPSP 410
DBL6A SVGEETLPPSP 410
BG8090 SVGEETLPPSP 410
L81905 SVGEETLPPSP 410

420
EF6796 SVGEETLPPSP 420
BG9163 SVGEETLPPSP 420
E134 SVGEETLPPSP 420
D39 SVGEETLPPSP 420
DBL6A SVGEETLPPSP 420
BG8090 SVGEETLPPSP 420
L81905 SVGEETLPPSP 420

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BG9163 NSKKEELTSKTKAEELTAAFEQFKKDDT 430
E134 NSKKEELTSKTKAEELTAAFEQFKKDDT 430
D39 NSKKEELTSKTKAEELTAAFEQFKKDDT 430
DBL6A NSKKEELTSKTKAEELTAAFEQFKKDDT 430
BG8090 NSKKEELTSKTKAEELTAAFEQFKKDDT 430
L81905 NSKKEELTSKTKAEELTAAFEQFKKDDT 430

440
EF6796 NSKKEELTSKTKAEELTAAFEQFKKDDT 440
BG9163 NSKKEELTSKTKAEELTAAFEQFKKDDT 440
E134 NSKKEELTSKTKAEELTAAFEQFKKDDT 440
D39 NSKKEELTSKTKAEELTAAFEQFKKDDT 440
DBL6A NSKKEELTSKTKAEELTAAFEQFKKDDT 440
BG8090 NSKKEELTSKTKAEELTAAFEQFKKDDT 440
L81905 NSKKEELTSKTKAEELTAAFEQFKKDDT 440

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BG9163 SVGEETLPPSP 450
E134 SVGEETLPPSP 450
D39 SVGEETLPPSP 450
DBL6A SVGEETLPPSP 450
BG8090 SVGEETLPPSP 450
L81905 SVGEETLPPSP 450

460
EF6796 SVGEETLPPSP 460
BG9163 SVGEETLPPSP 460
E134 SVGEETLPPSP 460
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BG9163 SVGEETLPPSP 470
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EF6796 SVGEETLPPSP 480
BG9163 SVGEETLPPSP 480
E134 SVGEETLPPSP 480
D39 SVGEETLPPSP 480
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BG8090 SVGEETLPPSP 480
L81905 SVGEETLPPSP 480

490
EF6796 SVGEETLPPSP 490
BG9163 SVGEETLPPSP 490
E134 SVGEETLPPSP 490
D39 SVGEETLPPSP 490
DBL6A SVGEETLPPSP 490
BG8090 SVGEETLPPSP 490
L81905 SVGEETLPPSP 490

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EF6796 SVGEETLPPSP 500
BG9163 SVGEETLPPSP 500
E134 SVGEETLPPSP 500
D39 SVGEETLPPSP 500
DBL6A SVGEETLPPSP 500
BG8090 SVGEETLPPSP 500
L81905 SVGEETLPPSP 500

510
EF6796 SVGEETLPPSP 510
BG9163 SVGEETLPPSP 510
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540
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D39 SVGEETLPPSP 550
DBL6A SVGEETLPPSP 550
BG8090 SVGEETLPPSP 550
L81905 SVGEETLPPSP 550

560
EF6796 SVGEETLPPSP 560
BG9163 SVGEETLPPSP 560
E134 SVGEETLPPSP 560
D39 SVGEETLPPSP 560
DBL6A SVGEETLPPSP 560
BG8090 SVGEETLPPSP 560
L81905 SVGEETLPPSP 560

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570
EF6796 SVGEETLPPSP 570
BG9163 SVGEETLPPSP 570
E134 SVGEETLPPSP 570
D39 SVGEETLPPSP 570
DBL6A SVGEETLPPSP 570
BG8090 SVGEETLPPSP 570
L81905 SVGEETLPPSP 570

580
EF6796 SVGEETLPPSP 580
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L81905 SVGEETLPPSP 580

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D39 SVGEETLPPSP 600
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BG9163 SVGEETLPPSP 610
E134 SVGEETLPPSP 610
D39 SVGEETLPPSP 610
DBL6A SVGEETLPPSP 610
BG8090 SVGEETLPPSP 610
L81905 SVGEETLPPSP 610

620
EF6796 SVGEETLPPSP 620
BG9163 SVGEETLPPSP 620
E134 SVGEETLPPSP 620
D39 SVGEETLPPSP 620
DBL6A SVGEETLPPSP 620
BG8090 SVGEETLPPSP 620
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D39 SVGEETLPPSP 630
DBL6A SVGEETLPPSP 630
BG8090 SVGEETLPPSP 630
L81905 SVGEETLPPSP 630

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E134 SVGEETLPPSP 640
D39 SVGEETLPPSP 640
DBL6A SVGEETLPPSP 640
BG8090 SVGEETLPPSP 640
L81905 SVGEETLPPSP 640

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BG9163 SVGEETLPPSP 650
E134 SVGEETLPPSP 650
D39 SVGEETLPPSP 650
DBL6A SVGEETLPPSP 650
BG8090 SVGEETLPPSP 650
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Fig. 13 (cont'd)



[illegible]

780

P E K P A P A P K P E T P E T

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L81905

Fig 13 (cont'd)

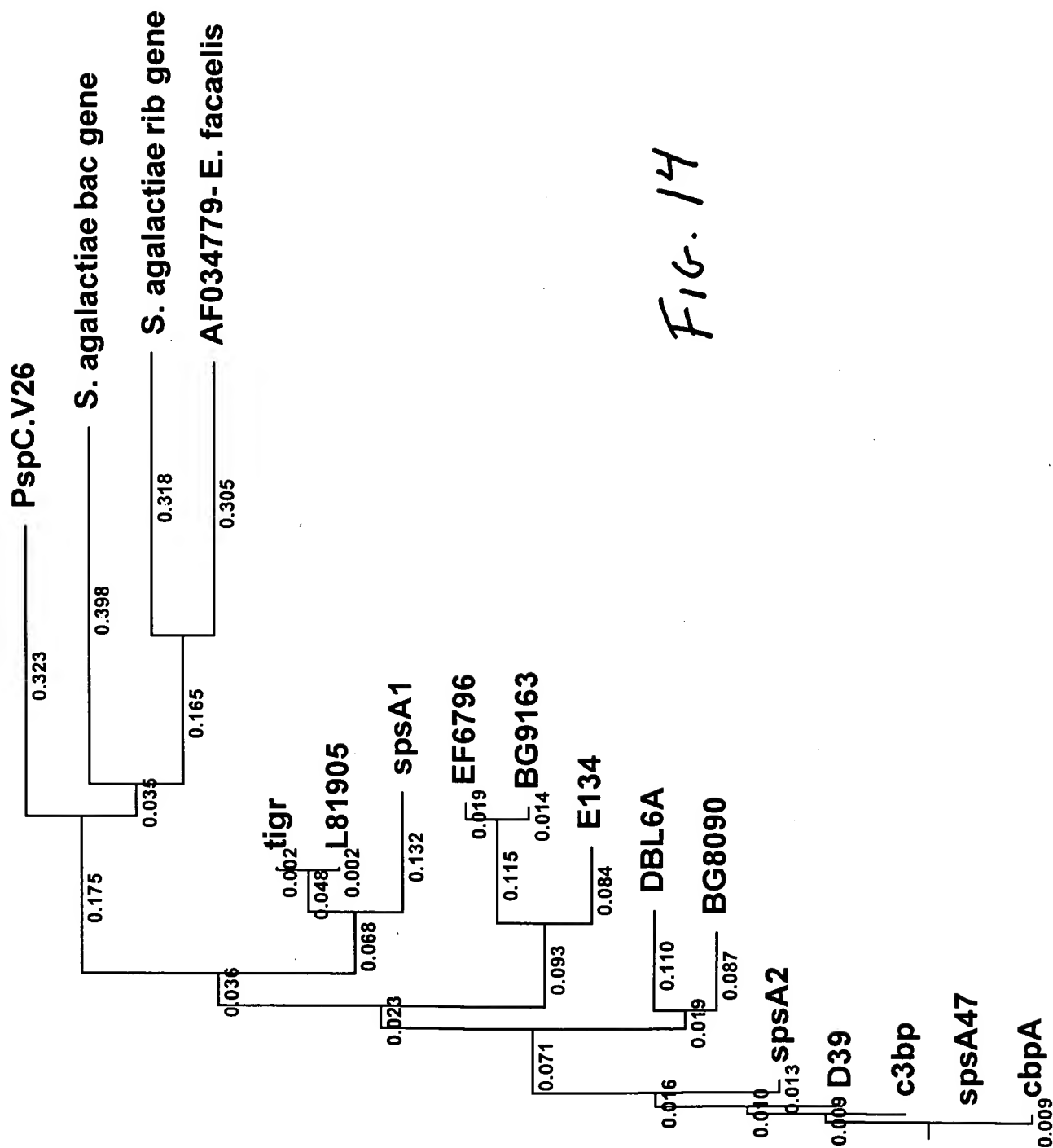


Fig. 14

ACCESSION -

**KEYWORDS** -

SOURCE -

SOURCE -	Location/Qualifiers
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FEATURES  
PROPEP <1..731

<1..731  
/note="3 to 2349 of V26.pspC (translated)"

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121 KEPELTKKLA EAEKKAKDQK EEDHRNYPTN TYKTIELEIA EAEVGVAKAE LELAQAQVQI  
181 PQDTEKINAA KAKVEAAKSN VKKLEKIKSD IEKTYLYKLD NSTKETPKSR VRRNSPQVGD  
241 SRELKETIDK AKETLSTY MV TRLTKLDPSV FWFADLLMDA KKVVEEYKTK LEDASDKKSV  
301 EDLRKEAEGK IESLIVTHQN REKENQAPQ PGGQAGGSMV VPPVTQTPTS TSQSPGQKAT  
361 EAEKKKLQDL IRQFQEALNK LDEDETKTPD GAKLTGEAGK AYNETRTRYAK EVVDKSKLL  
421 SQTAVTMDL AMQLTKLNDA MSKLKEAKAK LVPEVKPQPE NPEPKPQPEG EKPSVPDINQ  
481 EKEKAKLAIA TYMSKILDDI KKHHLKKEKH HQIVALIKDL DKLRKQALSE IDNVNTKVEI  
541 ENTVHKVFAD MDTVWTKFQK GLIQTNPQVP EAQRAQRYQR FQIHQKAPDT PQVPEAPKSP  
601 EVPKVPEAPK APDTPQVPEA PKSPEVPKVS DTPKAPDTPQ VPEAPKSPV PKVPEAPKAP  
661 DTPQVPEAPK SPEVPKVPDT PKAPDTPQVP EAPKAPDTPQ IPEAPAPETP APAPEAPKTG  
721 WKQENGMMWKG

1A

FIG. 15

LOCUS V26DNA.PSP 2349 BP SS-DNA SYN

DEFINITION Streptococcus pneumoniae PspC gene from strain V26

ACCESSION -

KEYWORDS -

SOURCE -

BASE COUNT 937 A 457 C 505 G 450 T 0 OTHER

ORIGIN -

1 AATTCGCCCT TCGACGAATA GCTGAAGAGG AAAAGCTATT ACATGAAGTT ATAATCCCAA  
61 ATGGAAGCAT AAAGAGATAA ATACAAAATT CGATTATAT ACAGTTCATA TTGAAGTGAT  
121 ATAGTAAGGC TAAAGAAAAA ATATAGAAGG AAATAAACAT GTTTGCATCA AAAAGCGAAA  
181 GAAAAGTACA TTATTCAATT CGTAAATTTA GTATTGGAGT AGCTAGTGTA GTAGTTGCTA  
241 GTTTGTTCTT AGGAGGAGTA GTTCACGCAG AAGAGGTTAG AAGAGGGAAT AACCTCACGG  
301 TTACATCTAG TGGGGATGAA GTCGAGTCGC ATTATCAAG TATATTGGAG AAGGTCAGAA  
361 AAAGTTTGA AAAAGATCGA CATACCCAAA ATGTCGACTT AATCAAAAAG TTGCAAGACA  
421 TTAAGAGAAC GTATTGTAT AATTAAAG AGAAGCCGGA AGCTGAGTTG ACGTCAAAAA  
481 CAAATAAAGA GTTAGACGCA GCTTTTGAGA AGTTTAAAA AGAACCGAGAA CTTACTAAAA  
541 AATTAGCAGA AGCTGAGAAA AAAGCCCAAGG ATCAAAAAGA AGAAGATCAC CGTAACCTACC  
601 CAACCAATAC TTACAAAACA ATCGAACTGG AAATTGCGGA AGCAGAAGTA GGGGTGCGCA  
661 AGGCAGAGCT TGAGCTTGCA CAAGCTCAAG TCCAAATACC TCAAGATACT GAGAAAATTA  
721 ATGCTGCTAA AGCTAAAGTA GAAGCTGCTA AAAGTAATGT TAAAAACTA GAAAAAATTA  
781 AATCAGATAT TGA AAAAACG TATTTGTATA AATTAGATAA CTC AACCAA GAAACGCCAA  
841 AATCTAGAGT CGGAAGAAAT TCTCCGCAAG TAGCGGATTC GAGAGAACTT AAGGAAACGA  
901 TAGACAAAGC GAAAGAAACT CTGTCTACCT ATATGGTAA CCGTTTAAACG AAGCTGGATC  
961 CATCTGTTTT TTGGTTTGCA GATCTTCTTA TGGATGCTAA GAAAGTTGTG GAAGAATACA  
1021 AGACAAAATT AGAGGATGCT TCAGATAAAA AATCGGTAGA AGACTTGCGA AAGGAAGCAG  
1081 AAGGAAAAAT AGAGTCTCTT ATCGTGACTC ACCAAATAG AGAAAAAGAA AACCAACCCAG  
1141 CACCCCAACC AGGAGGACAA GCAGGTGGT CAATGGTTGT ACCACCGGTG ACGCAAACAC  
1201 CTCCATCAAC TTCCCAAAGT CCAGGACAAA AGCGACCGA AGCTGAAAAG AAAAAGTTAC  
1261 AAGACTTGAT TCGTCAATTC CAAGAAGCCT TGAACAACT AGACGATGAA ACAAGACTG  
1321 TTCCAGATGG GGCTAAACTC ACAGGAGAG CTGGAAGAGC CTATAATGAG ACTAGAATTT  
1381 ATGCGAAAGA AGTTGTTGAC AAGAGCAAGA AGCTTCTATC ACAGACAGCA GTGACAATGG  
1441 ATGAATTGGC AATGCAATTA ACCAAATTGA ACGATGCCAT GTCTAAATTG AAAGAAGCTA  
1501 AAGCGAAATT GGTACCAGAG GTTAAACCAC AGCCGGAAA CCCAGAGCCA AAACCAACAAC  
1561 CAGAGGGTGA GAAACCAAGC GTACCAGATA TTAATCAGGA GAAAGAAAA GCTAAACTTG  
1621 CTATAGCAAC ATACATGAGC AAGATTTTAG ATGATATAA GAAACATCAT CTGAAGAAAG  
1681 AAAACATCA TCAGATTGTT GCTCTTATTA AGGACCTTGA TAACTTAGA AAGCAAGCAC  
1741 TTTCTGAAAT TGATAATGTA AATACCAAAG TAGAAATTGA GAATACAGTC CACAAGGTAT  
1801 TTGCAGACAT GGATACGGT GTTACTAAAT TCCAAAAGG CTTAATTCAG AACACACCGC  
1861 AGGTTCCAGA AGCCCAAAGA GCCCAGAGGT ACCAAAGGTT TCAGATACAC CAAAAGGCTC

Fig. 15 (cont'd)

1921 CGGACACACC GCAGGTTCCA GAAGCACCAA AGAGCCCAGA GTACCAAAG GTTCCAGAAG  
1981 CACCAAAGGC TCCGGACACA CCGCAAGTTC CGGAAGCACC AAAGAGCCCA GAGGTACCAA  
2041 AGGTTTCAGA TACACCAAAG GCTCCGGACA CACCGCAGGT TCCAGAAGCA CCAAAGAGCC  
2101 CAGAGGTACC AAAGGTTCCA GAAGCACCAA AGGCTCCGGA CACACCGCAA GTTCCGGAAG  
2161 CACCAAAGAG CCCAGAGGTA CCAAGGTTT CAGATACACC AAAGGCTCCG GACACACCCG  
2221 AGGTTCCAGA AGCACCAGG GCTCCAGACA CACCGCAAAT TCCGGAAGCA CCAGCTCCAG  
2281 AAAGTCCGGC TCCAGCTCCA GAAGCTCCA AACAGGCTG GAAACAAGAA AACGGTATGT  
2341 GGAAGGGCG

//

Fig. 15 (cont'd)

Fig. 16

LOCUS E134.DNA 2405 BP SS-DNA SYN ~~XXXXXXXXXX~~  
DEFINITION -  
ACCESSION -  
KEYWORDS -  
SOURCE -  
FEATURES Location/Qualifiers  
CDS 187..2405  
BASE COUNT 1046 A 386 C 505 G 468 T 0 OTHER  
ORIGIN -


1 CGGCCGCCAG TGTGATGGAT ATCTGCAGAA TTCGCCCTTC GACGAATAGC TGAAGAGGAA  
61 AAGCTATTAC ATGAAGTTAT AATCCCAAAT GGAAGCATAA AGAGATAAAT ACAAATTTCG  
121 ATTTATATAC AGTTCATATT GAAGTGATAT AGTAAGGTTA AAGAAAAAAT ATAGAAGGAA  
181 ATAAACATGT TTGCATCAAA AAGCGAAAGA AAAGTACATT ATTCAATTCG TAAATTTAGT  
241 ATTGGAGTAG CTAGTGTAGT AGTTGCTAGT CTTGTTATGG GAAGTGTGGT TCATGCGACG  
301 GAGAATGAGG GAATTACCCA AGTAGCCACT TCTTATAATA AGGCAAATGA AAGTCAGACA  
361 GAACATAGGA AAGCTGCTAA ACAAGTCGAT GAAGATATAA AAAAAATGTT GAGTGAGATC  
421 CAAGAATATA TAAAAAAAT GTTGAGTGAG ATCCAATTAG ATAAAAGAAA ACATACCCAA  
481 AATGTCAACT TAAACAGAAA GTTGAGCGCA ATTCAAACGA AGTATTTGTA TGAATTAAGA  
541 GTTTTAAAG AGAAGTCGAA AAAAGAAGAG TTGACGTCAA AAACAAAAAA AGAGTTAGAC  
601 GCAGCTTTTG AGAAGTTTAA AAAAGAACCA GAACTTACTA AAAAATTAGC AGAAGCTAAA  
661 CAAAAGCCA AGGCTCAAAA AGAAGAAGAT TTCCGTAAC TACCAACCAA TACTTACAAA  
721 ACGCTTGAAC TTGAAATTGC TGAGTTTCGAT GTGAAAGTTA AAGAAGCGGA GCTTGAAC TA  
781 GTAAAAGAGG AAGCTAAACC CCGAAACGAG GAAAAAATTA AGCAAGCAAA AGCGAAAGTT  
841 GAGAGTAAAA AAGCTGAGGC TACAAGGTTA GAAGAAATCA AGACAGAACG TAAAAAGCA  
901 GAAGAAGAAG CTAAACGAAA AGCAGAAGAA TCTGAGAAAA AAGCTGCTGA AGCCAAACAA  
961 AAAGTGGATA CTAAAGAGCA AGGTAAACCA AAGAGGCGGG CAAAACGAGG  
AGTTTCTGGA  
1021 GAGCTAGCAA CACCTGATAA AAAAGAAAAT GATGCGAAGT CTTGAGATTC TAGCGTAGGT  
1081 GAAGAACTC TTCCAAGCCC ATCCCTTAAT ATGGCAAATG AAAGTCAGAC AGAACATAGG  
1141 AAAGATGTCG ATGAATATAT AAAAAAATG TTGAGTGAGA TCCAATTAGA TAGAAGAAAA  
1201 CATACCCAAA ATGTCAACTT AAACATAAAG TTGAGCGCAA TTAACGAA GTATTTGTAT  
1261 GAATTAAGTG TTTTAAAGA GAACTCGAAA AAAGAAGAGT TGACGTCAA AACCAAAGCA  
1321 GAGTTAACCG CAGCTTTTGA GCAGTTTAAA AAAGATACAT TGAAACCAGA AAAAAAGGT  
1381 GCAGAAGCTG AGAAGAAGGT TGAAGAAGCT AAGAAAAAG CCAAGGATCA  
AAAAGAAGAA  
1441 GATCGCCGTA ACTACCCAAC CAATACTTAC AAAACGCTTG AACTTGAAAT TGCTGAGTCC  
1501 GATGTGAAAG TTA AAAAAGC GGAGCTTGAA CTAGTAAAAG AGGAAGCTAA CGAATCTCGA  
1561 AACGAGGAAA AAATTAAGCA AGCAAAAGAG AAAGTTGAGA GTAAAAAGC TGAGGCTACA  
1621 AGGTTAGAAA AAATCAAGAC AGATCGTAAA AAAGCAGAAG AAGAAGCTAA ACGAAAAGCA  
1681 GAAGAATCTG AGAAAAAGC TGCTGAAGCC AAACAAAAAG TGGATGCTGA AGAATATGCT  
1741 CTTGAAGCTA AAATCGCTGA GTTGAATAT GAAGTTCAGA GACTAGAAAA AGAGCTCAAA  
1801 GAGATTGATG AGTCTGACTC AGAAGATTAT CTTAAAGAAG GCCTCCGTGC TCCTCTTCAA  
1861 TCTAAATTGG ATACCAAAAA AGCTAACTA TCAAACTTG AAGAGTTGAG TGATAAGATT  
1921 GATGAGTTAG ACGCTGAAAT TGCAAACTT GAAGTTCAAC TTAAAGATGC TGAAGGAAAC  
1981 AATAATGTAG AAGCTACTT TAAAGAAGGT TTAGAGAAAA CTAAGTCTGA GAAAAAGCT  
2041 GAATTAGAAA AAGCTGAAGC TGACCTTAAG AAAGCAGTTG ATGAGCCAGA AACTCCAGCT  
2101 CCGGCTCCTC AACCAGCTCC AGCTCCAGAA AAACCAGCTG AAAAACCAGC  
TCCAGCTCCA  
2161 GCTCCAGAAA AACCAGCTCC AGCTCCAGAA AAACCAGCTG AAAAACCAGC  
TGAAAAACCA  
2221 GCTGAAGAAC CAGCTGAAAA ACCAGCTCCA GCTCCAGAAA AACCAGCTCC  
AACTCCAGAA  
2281 AAACCAGCTC CAACTCCAGA AACTCCAAAA ACAGGCTGGA AACAAGAAAA  
CGGTATGTGG

2341 TACTTCTACA ATACTGATGG TTCAATGGCA ACAGGCTGGC.TCCAAAACAA TGGTTCATGG  
2401 TACTA

//

*Fig. 16(cont'd)*

2341 TACTTCTACA ATACTGATGG TTCAATGGCA ACAGGCTGGC.TCCAAAACAA TGGTTCATGG  
2401 TACTA

LOCUS D39.DNA 2774 BP SS-DNA SYN   
DEFINITION -  
ACCESSION -  
KEYWORDS -  
SOURCE -  
FEATURES Location/Qualifiers  
CDS 362..2467  
BASE COUNT 1057 A 476 C 615 G 624 T 2 OTHER  
ORIGIN -

*Fig. 17*

1 CCAAGCTATT AGGTGACACT ATAGAATACT CAAGCTATGC ATCAAGCTTA TGCTTGTCAA  
61 TAATCACAAA TATGTAGATC ATATCTTGTT TAGGACAGTA AAACATCCTA ATTACTTTTT  
121 AAATATTCTT CCTGAGTTGA TTGGCTTGAC CTTGTTGAGT CATGCTTATG TGACTTTTGT  
181 TTTAGTTTTT CCAGTTTATG CAGTTATTTT GTATCGACGA ATAGCTGAAG AGGAAAAGCT  
241 ATTACATGAA GTTATAATCC CAAATGGAAG CATAAAGAGA TAAATACAAA ATTCGATTTA  
301 TATACAGTTC ATATTGAAGT AATATAGTAA GGTTAAAGAA AAAATATAGA AGGAAATAAA  
361 CATGTTTGCA TCAAAAAGCG AAAGAAAAGT ACATTATTCA ATTCGTAAAT TTAGTATTGG  
421 AGTAGCTAGT GTAGCTGTTG CCAGTCTTGT TATGGGAAGT GTGGTTCATG CGACAGAGAA  
481 CGAGGGAAGT ACCCAAGCAG CCACCTCTTC TAATATGGCA AAGACAGAAC ATAGGAAAGC  
541 TGCTAAACAA GTCGTCGATG AATATATAGA AAAAATGTTG AGGGAGATTC AACTAGATAG  
601 AAGAAAACAT ACCCAAATG TCGCCTTAAA CATAAAGTTG AGCGCAATTA AAACGAAGTA  
661 TTTGCGTGAA TTAAATGTTT TAGAAGAGAA GTCGAAAGAT GAGTTGCCGT CAGAAATAAA  
721 AGCAAAGTTA GACGCAGCTT TTGAGAAGTT TAAAAAGAT ACATTGAAAC CAGGAGAAAA  
781 GGTAGCAGAA GCTAAGAAGA AGGTTGAAGA AGCTAAGAAA AAAGCCGAGG ATCAAAAAGA  
841 AGAAGATCGT CGTAACTACC CAACCAATAC TTACAAAACG CTTGAACTTG AAATTGCTGA  
901 GTTCGATGTG AAAGTTAAAG AAGCGGAGCT TGAAGTAGTA AAAGAGGAAG CTAAAGAATC  
961 TCGAAACGAG GGCACAATTA AGCAAGCAAA AGAGAAAAGTT GAGAGTAAAA AAGCTGAGGC  
1021 TACAAGGTTA GAAAACATCA AGACAGATCG TAAAAAGCA GAAGAAGAAG CTAACGAAA  
1081 AGCAGATGGT AAGTTGAAGG AAGCTAATGT AGCGACTTCA GATCAAGGTA  
AACCAAAGGG  
1141 GCGGGCAAAA CGAGGAGTTC CTGGAGAGCT AGCAACACCT GATAAAAAAG  
AAATGATGC  
1201 GAAGTCTTCA GATTCTAGCG TAGGTGAAGA AACTCTTCCA AGCTCATCCC TGAAATCAGG  
1261 AAAAAAGGTA GCAGAAGCTG AGAAGAAGGT TGAAGAAGCT GAGAAAAAG  
CCAAGGATCA  
1321 AAAAGAAGAA GATCGCCGTA ACTACCCAAC CAATACTTAC AAAACGCTTG ACCTTGAAAT  
1381 TGCTGAGTCC GATGTGAAAG TTAAAGAAGC GGAGCTTGAA CTAGTAAAAG  
AGGAAGCTAA  
1441 GGAACCTCGA GACGAGGAAA AAATTAAGCA AGCAAAAGCG AAAGTTGAGA  
GTAAAAAAGC  
1501 TGAGGCTACA AGGTTAGAAA ACATCAAGAC AGATCGTAAA AAAGCAGAAG AAGAAGCTAA  
1561 ACGAAAAGCA GCAGAAGAAG ATAAAGTTAA AGAAAAACCA GCTGAACAAC CACAACCAGC  
1621 GCCGGCTACT CAACCAGAAA AACCAGCTCC AAAACCAGAG AAGCCAGCTG  
ACAACCAAAA  
1681 AGCAGAAAAA ACAGATGATC AACAAGCTGA AGAAGACTAT GCTCGTAGAT CAGAAGAAGA  
1741 ATATAATCGC TTGACTCAAC AGCAACCGCC AAAAAGTAA AAACCAGCAC AACCATCTAC  
1801 TCCAAAAACA GGCTGGAAAC AAGAAAACGG TATGTGGTAC TTCTACAATA CTGATGGTTC  
1861 AATGGCAACA GGATGGCTCC AAAACAACGG TTCATGGTAC TATCTAAACG CTAATGGTGC  
1921 TATGGCGACA GGATGGCTCC AAAACAATGG TTCATGGTAC TATCTAAACG CTAATGGTTC  
1981 AATGGCAACA GGATGGCTCC AAAACAATGG TTCATGGTAC TACCTAAACG CTAATGGTGC  
2041 TATGGCGACA GGATGGCTCC AATACAATGG TTCATGGTAC TACCTAAACA  
GCAATGGCGC  
2101 TATGGCGACA GGATGGCTCC AATACAATGG CTCATGGTAC TACCTCAACG  
CTAATGGTGA  
2161 TATGGCGACA GGATGGCTCC AAAACAACGG TTCATGGTAC TACCTCAACG



CTAATGGTGA

2221 TATGGCGACA GGATGGCTCC AATACAACGG TTCATGGTAT TACCTCAACG CTAATGGTGA

2281 TATGGCGACA GGTTGGGTGA AAGATGGANA TACCTGGTAC TATCTTAAAG

CATCAGGTGC

2341 TATGAAAGCA AGCCAATGGT TCAAAGTATC AGATAAATGG TACTATGTCA ATGGCTCAGG

2401 TGCCCTTGCA GTCAACACAA CTGTAGATGG CTATGGAGTC AATGCCAATG

GTGAATGGGT

2461 AAATAAACC TAATATAACT AGTTAATACT GACTTCCTGT AAGAACTTTT TAAAGTATTC

2521 CCTACAAATA CCATATCCTT TCAGTAGATA ATATACCCTT GTAGGAAGTT TAGATTAAAA

2581 AATAACTCTG TAATCTCTAG CCGGATTTAT AGCGCTAGAG ACTACGGAGT TTTTTTGATG

2641 AGGAAAGAAT GCGGGCATTG AAGAGACTCT TTAAGAGAGT TACGGGTTTT AAATAATTAA

2701 GCCTTCTCCA ATTGCAAGAG GGCTTCAATC TCTGCTAGGG TGCTAGCTTG

CGAAATGGCT

2761 CCACGGAGTT TNGC

//

*Fig. 17 (cont'd)*

LOCUS BG9163.DNA 2489 BP SS-DNA

SYN

Fig. 18

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

CDS 221..2489

BASE COUNT 1026 A 429 C 541 G 493 T 0 OTHER

ORIGIN -

1 GATTGTATAC GACCACTATA GGGCGAATTG GGCCCGACGT CGCATGCTCC CGGCCGCCAT  
61 GGCCGCGGGT ATTCGACGAA TAGCTGAAGA GGAAAAGCTA TTACATGAAG TTATAATCCC  
121 AAATGGAAGC ATAAAGAGAT AAATACAACA TTCGATTTAT ATACAGTTCC TATTGAAGTG  
181 ATATAATAAG GTTAAAGAAA AAATATAGAA GGAAATAAAC ATGTTTGCAT CAAAAGCGA  
241 AAGAAAAGTA CATTATTCAA TTCGTAAATT TAGTATTGGA GTAGCTAGTG TAGCTGTTGC  
301 CAGCTTGTTT TTAGGAGGAG TAGTCCATGC AGAAGGGGTT AGAAGTGGGA ATAACCTCAC  
361 GGTTACATCT AGTGGGCAAG ATATATCGAA GAAGTATGCT GATGAAGTCG AGTCGCATCT  
421 AGAAAGTATA TTGAAGGATG TCAAAAAAAA TTTGAAAAA GTTCAACATA CCCAAATGT  
481 CGGCTTAATT ACAAAGTTGA GCGAAATTAA AAAGAAGTAT TTGTATGACT TAAAAGTTAA  
541 TGTTTTATCG GAAGCTGAGT TGACGTCAA AACAAAAGAA ACAAAGAAA AGTTAACCGC  
601 AACTTTTGAG CAGTTTAAAA AAGATACATT ACCAACAGAA CCAGAAAAAA AGGTAGCAGA  
661 AGCTCAGAAG AAGGTTGAAG AAGCTAAGAA AAAAGCCGAG GATCAAAAAG AAAAGATCG  
721 CCGTAACCTAC CCAACCATTA CTTACAAAAC GCTTGAACCT GAAATTGCTG AGTCCGATGT  
781 GGAAGTTAAA AAAGCGGAGC TTGAACTAGT AAAAGTGAAA GCTAAGGAAT CTCAAGACGA  
841 GGAAAAAATT AAGCAAGCAG AAGCGGAAGT TGAGAGTAAA CAAGCTGAGG CTACAAGGTT  
901 AAAAAAATC AAGACAGATC GTGAAGAAGC TAAACGAAAA GCAGATGCTA AGTTGAAGGA  
961 AGCTGTTGAA AAGAATGTAG CGACTTCAGA GCAAGATAAA CCAAAGAGGC

GGGCAAAACG

1021 AGGAGTTTCT GGAGAGCTAG CAACACCTGA TAAAAAGAA AATGATGCGA AGTCTTCAGA  
1081 TTCTAGCGTA GGTGAAGAAA CTCTTCCAAG CCCATCCCTT AATATGGCAA ATGAAAGTCA  
1141 GACAGAACAT AGGAAAGATG TCGATGAATA TATAAAAAA ATGTTGAGTG AGATCCAATT  
1201 AGATGGAAGA AACATACCC CAAATGTCAA CTTAAACATA AAGTTGAGCG CAATTTAAAC  
1261 GAAGTATTTG TATGAATTAA GTGTTTTAAA AGAGAACTCG AAAAAAGAAG AGTTGACGTC  
1321 AAAAACCAAA GCAGAGTTAA CCGCAGCTTT TGAGCAGTTT AAAAAAGATA CATTGAAACC  
1381 AGAAAAAATA GTAGCAGAAG CTGAGAAGAA GGTTGAAGAA GCTAAGAAAA

AAGCCAAGGA

1441 TCAAAAAGAA GAAGATCGCC GTAACCTACC AACCAATACT TACAAAACGC TTGAACTTGA  
1501 AATTGCTGAG TCCGATGTGA AAGTTAAAGA AGCGGAGCTT GAACTAGTAA

AAGAGGAAGC

1561 TAACGAATCT CGAAACGAGG AAAAAATTAA GCAAGCAAAA GAGAAAGTTG AGAGTAAAAA  
1621 AGCTGAGGCT ACAAGGTTAG AAAAAATCAA GACAGATCGT AAAAAAGCAG AAGAAGAAGC  
1681 TAAACGAAAA GCAGAAGAAT CTGAGAAAAA AGCTGCTGAA GCCAAACAAA AAGTGGATGC  
1741 TGAAGAATAT GCTCTTGAAG CTAAAATCGC TGAGTTGGAA TATGAAGTTC AGAGACTAGA  
1801 AAAAGAGCTC AAAGAGATTG ATGAGTCTGA CTCAGAAGAT TATCTTAAAG AAGGCCTCCG  
1861 TGCTCCTCTT CAATCTAAAT TGGATACCAA AAAAGCTAAA CTATCAAAAC TTGAAGAGTT  
1921 GAGTGATAAG ATTGATGAGT TAGACGCTGA AATTGCAAAA CTTGAAGTTC AACTTAAAGA  
1981 TGCTGAAGGA AACAATAATG TAGAAGCCTA CTTTAAAGAA GGTTTAGAGA AACTACTGCT  
2041 TGAGAAAAAA GCTGAATTAG AAAAAGCTGA AGCTGACCTT AAGAAAGCAG TTGATGAGCC  
2101 AGAAACTCCA GCTCCGGCTC CTCAACCAGC TCCGGCTCCA GAAAAACCAG

CTGAAAAACC

2161 AGCTCCAGCT CCAGCTCCAG AAAAACCAGC TCCAGCTCCA GAAAAACCAG

CTCCAGCTCC

2221 AGAAAAACCA GCTCCAGCTC CAGAAAAACC AGCTCCAGCT CCAGAAAAAC

CAGCTCCAGC

2281 TCCAGAAAAA CCAGCTCCAG CTCCAGAAAA ACCAGCTCCA GCTCCTAAAC CAGAAACTCC

2341 AGAAACAGGC TGGAAACAAG AAAACGGTAT GTGGTACTTC TACAATACTG ATGGTTCAAT  
2401 GGCAACAGGC TGGCTCCAAA ACAATGGCTC ATGGTACTAC CTCAACAGCA  
ATGGCGTTAT  
2461 GGCGACAGGA TGGTTCCCAA ACAATGGTC  
//

*Fig. 18 (cont'd)*

LOCUS BG8090.DNA 1680 BP SS-DNA

SYN

Fig. 19

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

CDS 220..1680

BASE COUNT 714 A 287 C 375 G 304 T 0 OTHER

ORIGIN -

1 ATTGTATACG ACTCACTATA GGGCGAATTG GGCCCGACGT CGCATGCTCC CGGCCGCCAT  
61 GGCCGCGGGA TTCGACGAAT AGCTGAAGAG GAAAAGCTAT TACATGAAGT TATAATCCCA  
121 AATGGAAGCA TAAAGAGATA AATACAAAAT TCGATTATA TACAGTTCAT ATTGAAGTGA  
181 TATAGTAAGG TTAAAGAAAA AATATAGAAG GAAATAACA TGTTCATC AAAAAACGAA  
241 AGAAAAGTAC ATTATTCAAT TCGTAAATTT AGTATTGGAG TAGCTAGTGT AGCTGTTGCC  
301 AGTCTTTTTA TGGGAAGTGT GGTTCATGCG ACAGAGAAGG AGGTAAGTAC CCAAGTAGCC  
361 ACTTCTTTTA ATAAGGCAAA TAAAGTCAG ACAGAACATA TGAAAGCTGC TAAACAAGTC  
421 GATGAATATA TAACAAAAAA GCTCCAATTA GATAGAAGAA AACATACCCA AAATGTCGGC  
481 TTAATCACAA AGTTGGGCGT AATTAAAACG GAGTATTTGC ATAGATTAAG TGTTCAAAA  
541 GAGAAGTCGG AAGCTGAGTT GCCGTCAGAA ATAAAAGCAA AGTTAGACGC AGCTTTTGAG  
601 CAGTTTAAAA AAGATACATT ACCAACAGAA CCAGGAAAAA AGGTAGCAGA AGCTGAGAA  
661 AAGGTTGAAG AAGCTAAGAA AAAAGCCGAG GATCAAAAAG AAGAAGATCG TCGTAAGTAC  
721 CCAACCATTA CTTACAAAAC GCTTGAAGTT GAAATTGCTG AGTCCGATGT GGAAGTTAAA  
781 AAAGCGGAGC TTGAAGTAGT AAAAGAGGAA GCTAAGGGAT CTCGAAACGA GCAAAAAGTT  
841 AACCAAGCAA AAGCGAAAAG TGAGAGTAAA CAAGCTGAGG CTACAAGTT AAAAAAATC  
901 AAGACAGATC GTGAACAAGC TGAGACTACA AGGTTAGAAA ACATCAAGAC AGATCGTGAA  
961 AAAGCAGAAG AAGCTAAACG AAAAGCAGAT GCTAAAGAGC AAGATGAATC  
AAAGAGGCGG  
1021 GTAAAAGGAG GAGTTCCGGG AGAGCAAGCA AACTTGATA AAAAAGAAAA  
TGATGCGAAG  
1081 TCTTCAGATT CTAGCGTAGG TGAAGAACT CTTCCAAGCC CATCCCTGAA ATCAGGAAAA  
1141 AAGGTAGCAG AAGCTGAGAA GAAGGTTGCA GAAGCTGAGA AAAAAGCCAA  
GGATCAAAAA  
1201 GAAGAAGATC GCCGTAAC TAACCAACCAAT ACTTACAAAA CGCTTGAAGT TGAAATTGCT  
1261 GAGTCCGATG TGAAAGTTAA AGAAGCGGAG CTTGAACTAG TAAAGAGGA  
AGCTAAGGAA  
1321 TCTCGAAACG AGGAAAAAGT TAAGCAAGCA AAAGCGGAAG TTGAGAGTAA  
AAAAGCTGAG  
1381 GCTACAAGGT TAGAAAAAAT CAAGACAGAT CGTAAAAAAG CAGAAGAAGC TAAACGAAAA  
1441 GCAGCAGAAG AAGATAAAGT TAAAGAAAAA CCAGCTGAAC AACCACAACC  
AGCGCCGGCT  
1501 CCTCAACCAG AAAAACCAGC TCCAGCTCCA AAACCAGAGA ATCCAGCTGA ACAACCAAAA  
1561 GCAGAAAAAC CAGCTGATCA ACAAGCTGAA GAAGACTATG CTCGTAGATC AGAAGAAGAA  
1621 TATAATCGCT TGAATCAACA GCAACCGCCA AAAACTGAAA AACCAGCACA ACCATCTACT

//

LOCUS L81905.DNA 1766 BP SS-DNA

SYN

Fig. 20

DEFINITION -

ACCESSION -

KEYWORDS -

SOURCE -

FEATURES Location/Qualifiers

CDS 217..1766

BASE COUNT 741 A 313 C 402 G 309 T 1 OTHER

ORIGIN -

1 GTATACGACT CACTATAGGG CGAATTGGGC CCGACGTCGC ATGCTCCCGG  
CCGCCATGGC

61 CGCGGGATTG GACGAATAGC TGAAGAGGAA AAGCTATTAC ATGAAGTTAT AATCCCAAAT  
121 GGAAGCATAA AGAGATAAAT ACAAATTCG ATTTATATAC AGTTCATATT GAAGTGATAT  
181 AGTAAGGTTA AAGAAAAAAT ATAGAAGGAA ATAAACATGT TTGCATCAA AAGCGAAAGA  
241 AAAGTACATT ATTCAATTCG TAAATTTAGT GTTGGAGTAG CTAGTGTAGT TGTGCCAGT  
301 CTTGTTATGG GAAGTGTGGT TCATGCGACA GAGAACGAGG GAGCTACCCA

AGTACCCACT

361 TCTTCTAATA GGGCAAATGA AAGTCAGGCA GAACAAGGAG AACAACTAA AAAACTCGAT  
421 TCAGAACGAG ATAAGGCAAG GAAAGAGGTC GAGGAATATG TAAAAAAT AGTGGGTGAG  
481 AGCTATGCAA AATCAACTAA AAAGCGACAT ACAATTACTG TAGCTCTAGT TAACGAGTTG  
541 AACACATTA AGAACGAGTA TTTGAATAAA ATAGTTGAAT CAACCTCAGA AAGCCAACTA  
601 CAGATACTGA TGATGGAGAG TCGATCAAAA GTAGATGAAG CTGTGTCTAA GTTTGAAAAG  
661 GACTCATCTT CTTGTCAGG TTCAGACTCT TCCACTAAAC CGGAAGCTTC AGATACAGCG  
721 AAGCCAAACA AGCCGACAGA ACCAGGAGAA AAGGTAGCAG AAGCTAAGAA

GAAGGTTGAA

781 GAAGCTGAGA AAAAAGCCAA GGATCAAAAA GAAGAAGATC GTCGTAACCTA CCCAACCATT  
841 ACTTACAAAA CGCTTGAAGT TGAAATTGCT GAGTCCGATG TGGAAGTTAA AAAAGCGGAG  
901 CTTGAAGTAG TAAAAGTGAA AGCTAACGAA CCTCGAGACG AGCAAAAAAT TAAGCAAGCA  
961 GAAGCGGAAG TTGAGAGTAA ACAAGCTGAG GCTACAAGGT TAAAAAAT CAAGACAGAT  
1021 CGTGAAGAAG CAGAAGAAGA AGCTAAACGA AGAGCAGATG CTAAAGAGCA

AGGTAAACCA

1081 AAGGGGCGGG CAAAACGAGG AGTTCCTGGA GAGCTAGCAA CACCTGATAA

AAAAGAAAAT

1141 GATGCGAAGT CTTGAGATTC TAGCGTAGGT GAAGAACTC TTCCAAGCCC ATCCCTGAAA  
1201 CCAGAAAAAA AGGTAGCAGA AGCTGAGAAG AAGGTTGAAG AAGCTAAGAA

AAAAGCCGAG

1261 GATCAAAAAG AAGAAGATCG CCGTAACCTAC CCAACCAATA CTTACAAAAC GCTTGAAGTT  
1321 GAAATTGCTG AGTCCGATGT GGAAGTTAAA AAAGCGGAGC TTGAACTAGT AAAAGAGGAA  
1381 GCTAAGGAAC CTCGAAACGA GGAAAAAGTT AAGCAAGCAA AAGCGGAAGT

TGAGAGTAAA

1441 AAAGCTGAGG CTAAGAGTT AGAAAAATC AAGACAGATC GTAAAAAGC AGAAGAAGAA  
1501 GCTAAACGAA AAGCAGCAGA AGAAGATAAA GTTAAAGAAA AACCAGCTGA ACAACCACAA  
1561 CCAGCGCCGG CTCCAAAAGC AGAAAAACCA GCTCCAGCTC CAAAACCAGA

GAATCCAGCT

1621 GAACAACCAA AAGCAGAAAA ACCAGCTGAT CAACAAGCTG AAGAAGAGTA TGCTCGTAGA  
1681 TCAGAAGAAG AATATAATCG CTTGACTCTA CAGCAACCGC CAAAACTGA AAAACCAGCA  
1741 CAACCATCTA CTCCAAAAC AAANAC

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LOCUS DBL6A.DNA 1590 BP SS-DNA SYN   
DEFINITION -  
ACCESSION -  
KEYWORDS -  
SOURCE -  
FEATURES Location/Qualifiers  
CDS 127..1590  
BASE COUNT 701 A 261 C 339 G 288 T 1 OTHER  
ORIGIN -

Fig. 21

1 AAACATTAC ATGAAGTTAT AATCCCAAAT GGAAGCATAA AGAGATAAAT ACAAAATTCTG  
61 ATTTATATAC AGTTCATATT GAAGTGATAT AGTAAGGTTA AAGAAAAAAT ATAGAAGGAA  
121 ATAATTATGT TTGCATCYAA AAGCGAAAGA AAAGTACATT ATTCAATTCTG TAAATTTAGT  
181 ATTGGAGTAG CTAGTGATAGC TGTTGCTAGC TTGTTCTTAG GAGGAGTAGT CCATGCAGAA  
241 GGGGTTAGAA GTGAGAATAC CCCCAGGTT ACATCTAGTG GGGATGAAGT CGATGAATAT  
301 ATAAAAAATA TGTTGAGTGA GATCCAATTA GATAAAAGAA AACATACCCA CAATTTCTGCC  
361 TTAACCTAA AGTTGAGCAG AATTAACG GAGTATTTGT ATAAATTAAGTAAATGTT  
421 TTAGAAGAAA AGTCAAAAGC TGAGTTGACG TCAAAAACAA AAAAGAGGT AGACGCAGCT  
481 TTTGAGAAGT TTAAGAAAGA TACATTGAAA CTAGGAGAAA AGGTAGCAGA AGCTCAGAAG  
541 AAGGTTGAAG AAGCTAAGAA AAAAGCCAAG GATCAAAAAG AAGAAGATCA CCGTAAGTAC  
601 CCAACCAATA CTTACAAAAC GCTTGAACCT GAAATTGCTG AGTCCGATGT GAAAGTTAAA  
661 GAAGCGGAGC TTGAACCTATT GAAAGAGGAA GCTAAACTC GAAACGAGGA CACAATTAAC  
721 CAAGCAAAAG CGAAAGTTAA GAGTGAACAA GCTGAGGCTA CAAGGTTAAA AAAAATCAAG  
781 ACAGATCGTG AACAAGCTGA GGCTACAAGG TTAGAAAACA TCAAGACAGA TCGTGAAAAA  
841 GCAGAAGAAG CTAAACGAAA AGCAGAAGCA GAAGAAGTTA AAGATAAACT AAAGAGGCGG  
901 ACAAACGAG CAGTTCCTGG AGAGCCAGCA ACACCTGATA AAAAGAAAAA TGATGCGAAG  
961 TCTTCAGATT CTAGCGTAGG TGAAGAACT CTTCAAGCC CATCCCTGAA ATCAGGAAAA  
1021 AAGGTAGCAG AAGCTCAGAA GAAGGTAGCA GAAGCTGAGA AAAAGCCAA  
GGATCAAAAA  
1081 GAAGAAGATC GCCGTAACCTA CCAACCAAT ACTTACAAAA CGCTTGACCT TGAAATTGCT  
1141 GAGTCCGATG TGAAAGTTAA AGAAGCGGAG CTTGAAGTAG TAAAGAGGA  
AGCTAAGGAA  
1201 TCTCGAAACG AGGAAAAAGT TAAGCAAGCA AAAGCGAAAG TTGAGAGTAA AAAAGCTGAG  
1261 GCTACAAGGT TAGAAAAAAT CAAGACAGAT CGTAAAAAG CAGAAGAAGC TAAACGAAGA  
1321 GCAGCAGAAG AAGATAAAGT TAAAGAAAAA CCAGCTGAAC AACCACAACC  
AGCGCCGGCT  
1381 CCTCAACCAG AAAAACCAAC TGAAGAGCCT GAGAATCCAG CTCCAGCTCC  
AAACCTGAG  
1441 AATCCAGCTG AACAACCAAA AGCAGAAAAA CCAGCTGATC AACAAGCTGA AGAAGACTAT  
1501 GCTCGTAGAT CAGAAGAAGA ATATAATCGC TTGACTCAAC AGCAACCGCC AAAAAGTAA  
1561 AAACCAGCAC AACCATCTAC TCAAAAAACA

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